

GenCore version 5.1.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2006, 22:34:29 ; Search time 1421 Seconds
(without alignments)
12207.568 Million cell updates/sec

Title: US-10-719-024-1
Perfect score: 2488
Sequence: 1 aaaaatgcagcgcgaaaaa.....aaataaactgcataacaa 2488

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_8.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002as.*
 - 7: Geneseqn2002bs.*
 - 8: Geneseqn2003as.*
 - 9: Geneseqn2003bs.*
 - 10: Geneseqn2003cs.*
 - 11: Geneseqn2003ds.*
 - 12: Geneseqn2004as.*
 - 13: Geneseqn2004bs.*
 - 14: Geneseqn2005s.*
 - 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488	100.0	2488	14	ADY61074 D melanog
2	2488	100.0	2488	14	ABE53800 Drosophil
C 3	2488	100.0	4483	4	ABL07558 Drosophil
C 4	2488	100.0	18737	4	ABL07492 Drosophil
C 5	2488	100.0	18737	4	ABL07530 Drosophil
6	2483	99.8	2483	4	ABL07559 Drosophil
7	2238.2	90.0	2304	2	AAQ14176 Clone pXR
8	2238.2	90.0	2304	2	AAQ55374 pXR2C8 DN
9	2238.2	90.0	2304	2	AAT76787 Insect XR
10	2238.2	90.0	2304	2	AAT89959 D. melano
11	825	33.2	825	6	ABE68157 Drosophil
12	825	33.2	825	6	ABT08312 ECR-based
13	799	32.1	799	8	ACC00562 Drosophila
14	799	32.1	799	9	ACC71950 D. melano
15	488.6	19.6	1536	4	AAF32133 L. cuprina
16	488.6	19.6	1596	4	AAF32132 L. cuprina
17	488.6	19.6	2453	4	AAF32131 L. cuprina
18	454.4	18.3	1377	2	AAX90667 L. cuprin

19	243	9.8	4375	4	AAS15657	Aas15657 Spruce bu
20	243	9.8	4375	6	ABS70120	Abs70120 Spruce bu
21	239.2	9.6	1837	3	AAA10313	Aaa10313 European
22	232.6	9.3	1344	8	ACA05056	Aca05056 Flea ultr
C 23	232.6	9.3	1344	8	ACA05057	Aca05057 Flea ultr
C 24	232.6	9.3	1344	13	ADU48280	Adu48280 Ctenoceph
25	232.6	9.3	1344	13	ADU48278	Adu48278 Ctenoceph
26	232.6	9.3	1422	8	ACA05060	Aca05060 Flea ultr
C 27	232.6	9.3	1422	8	ACA05061	Aca05061 Flea ultr
28	232.6	9.3	1422	13	ADU48284	Adu48284 Ctenoceph
C 29	232.6	9.3	1422	13	ADU48286	Adu48286 Ctenoceph
C 30	232.6	9.3	1749	8	ACA05055	Aca05055 Flea ultr
31	232.6	9.3	1749	8	ACA05054	Aca05054 Flea ultr
32	232.6	9.3	1749	13	ADU48275	Adu48275 Ctenoceph
C 33	232.6	9.3	1749	13	ADU48277	Adu48277 Ctenoceph
C 34	232.6	9.3	1975	8	ACA05059	Aca05059 Flea ultr
35	232.6	9.3	1975	8	ACA05058	Aca05058 Flea ultr
36	232.6	9.3	1975	13	ADU48281	Adu48281 Ctenoceph
C 37	232.6	9.3	1975	13	ADU48283	Adu48283 Ctenoceph
38	222.2	8.9	1398	6	ABA95998	Aba95998 Heliothis
39	219.6	8.8	2951	8	AD47611	Ad47611 Heliothis
C 40	218	8.8	1421	8	ACA05052	Aca05052 Flea ultr
41	218	8.8	1421	8	ACA05051	Aca05051 Flea ultr
C 42	218	8.8	1421	13	ADU48273	Adu48273 Ctenoceph
43	218	8.8	1421	13	ADU48272	Adu48272 Ctenoceph
44	216.4	8.7	943	8	ACA05066	Aca05066 Flea ultr
C 45	216.4	8.7	943	8	ACA05067	Aca05067 Flea ultr

ALIGNMENTS

RESULT 1

ADY61074
ID ADY61074 standard; cDNA; 2488 BP.

XX AC ADY61074;

XX DT 19-MAY-2005 (first entry)

XX DE D melanogaster ultraspiracle (USP) wild-type cDNA SeqID1.

XX KW protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX KW gene; ss; ultraspiracle; USP.

XX OS Drosophila melanogaster.

XX FH Key Location/Qualifiers
XX CDS 371..1897

FT FT /*tag= a
FT FT /product= "D melanogaster ultraspiracle (USP) wild-type
FT FT protein"

XX PN US2005054569-A1.

XX PD 10-MAR-2005.

XX PF 24-NOV-2003; 2003US-00719024.

XX PR 22-NOV-2002; 2002US-0428282P.

XX PA (JONE/) JONES G.

XX PA (JONE/) JONES D.

XX PI Jones G, Jones D;

XX DR WPI; 2005-221953/23.

XX PT P-PSDB; ADY61075.

XX PT New mutant hormone receptor nucleic acids useful in the fields of drug
XX PT discovery and pest control, in particular for identifying chemical
XX PT compounds in activating or blocking particular hormone-dependent pathways
XX PT in various organisms.

XX Claim 1; SEQ ID NO 1; 35pp; English.

XX This invention relates to novel mutant nuclear hormone receptors and the
CC DNA sequences which encode them. The invention may be useful for the
CC development of compounds with a pesticide activity acting as hormone
CC receptor agonists or antagonists. The methods and compositions of the
CC present invention are useful in the fields of drug discovery and pest
CC control, in particular for providing biochemical tools and assays to
CC identify ligands of nuclear hormone receptors and identifying a pest
CC control agent. The present sequence is that of the D melanogaster
CC ultrastructural (usp) wild-type cDNA which was used during the development
CC of the novel mutant nuclear hormone receptors of the invention.

XX SQ Sequence 2488 BP; 669 A; 669 C; 648 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2488; DB 14; Length 2488;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAATGTCGAGCGGAAAAAGGTAATTTATTCATAGTCAGAAAGTCGGCAATCTTTGT 60
Db |||||
Qy 61 TTGTTGGTAAAGCGCAATTTGTTGGAGCGAGCGAATAAGTCGCGTCTCCATCGGC 120
Db |||||
Qy 61 TTGTTGGTAAAGCGCAATTTGTTGGAGCGAGCGAATAAGTCGCGTCTCCATCGGC 120
Db |||||
Qy 121 TCAAGATTATGTAATGACGACACACCCCAACCAACGAAACTGCAACTGCTCCACT 180
Db |||||
Qy 121 TCAAGATTATGTAATGACGACACACCCCAACCAACGAAACTGCAACTGCTCCACT 180
Db |||||
Qy 181 TGGCCCAACGACCAATAGCGGACGGACGGACACGGTGGCGTTGGCAAGTGAACCCCA 240
Db |||||
Qy 181 TGGCCCAACGACCAATAGCGGACGGACGGACACGGTGGCGTTGGCAAGTGAACCCCA 240
Db |||||
Qy 241 ACAGAGCGCAAGCGAGCGCAAGACACACACATACACAGAGAAACAGCAAGAG 300
Db |||||
Qy 241 ACAGAGCGCAAGCGAGCGCAAGACACACACATACACAGAGAAACAGCAAGAG 300
Db |||||
Qy 301 AAACCGGTAGGCGGAGGAGGCGTCCGCCCAAGTTCTCCTCAATATACCCAGACCAATCA 360
Db |||||
Qy 301 AAACCGGTAGGCGGAGGAGGCGTCCGCCCAAGTTCTCCTCAATATACCCAGACCAATCA 360
Db |||||
Qy 361 CAAGCCCAAGATGGAACAATCGGACGACGACGACGACGACGACGACGACGACGACGAC 420
Db |||||
Qy 361 CAAGCCCAAGATGGAACAATCGGACGACGACGACGACGACGACGACGACGACGACGAC 420
Db |||||
Qy 421 GGAGGTCAAGCGGACATCTCGAGCTGAAACAGCAACAGCAACAGCACTTTGCGCCAA 480
Db |||||
Qy 421 GGAGGTCAAGCGGACATCTCGAGCTGAAACAGCAACAGCAACAGCACTTTGCGCCAA 480
Db |||||
Qy 481 GGCGGAGATCCCGTCCCTTCATGCGGCGCATGTCCATGTGTCACGTGTCGCGGCTC 540
Db |||||
Qy 481 GGCGGAGATCCCGTCCCTTCATGCGGCGCATGTCCATGTGTCACGTGTCGCGGCTC 540
Db |||||
Qy 541 CAACTCCGCGAGCTCAACAAACAGCGCTGAGATGCCCAATGGGCGAGGCGCCCA 600
Db |||||
Qy 541 CAACTCCGCGAGCTCAACAAACAGCGCTGAGATGCCCAATGGGCGAGGCGCCCA 600
Db |||||
Qy 601 TTCGGCTGAGGCTCTGCGCGCGTGCAGTCCAGCAGCATATCCGCTCAACCATCCGCT 660
Db |||||
Qy 601 TTCGGCTGAGGCTCTGCGCGCGTGCAGTCCAGCAGCATATCCGCTCAACCATCCGCT 660
Db |||||
Qy 661 GAGCGGCAAGCAAGCACTCTGCTCTATTTGCGGGATCGGGCCAGTGGCAAGCACTAGGG 720
Db |||||
Qy 661 GAGCGGCAAGCAAGCACTCTGCTCTATTTGCGGGATCGGGCCAGTGGCAAGCACTAGGG 720
Db |||||
Qy 721 CGGTACAGCTGTGAGGCTGCAAGGCTCTTTTAAACGACAGTGGCGGAGGATCTCAC 780
Db |||||
Qy 721 CGGTACAGCTGTGAGGCTGCAAGGCTCTTTTAAACGACAGTGGCGGAGGATCTCAC 780
Db |||||
Qy 781 ATACGCTTGCAGGAGAACCGCAACTGTCATCATAGACAGCGGAGGAGGACCGCTGCCA 840
Db |||||

Db |||||
Qy 781 ATACGCTTGCAGGAGAACCGCAACTGTCATCATAGACAGCGCAGAGAACCGCTGCCA 840
Db |||||
Qy 841 GTACTCCGCTACAGAGTGCCTTAACCTCGGCGCATGAAGCGGAGCGGTCCAGGAGGA 900
Db |||||
Qy 841 GTACTCCGCTACAGAGTGCCTTAACCTCGGCGCATGAAGCGGAGCGGTCCAGGAGGA 900
Db |||||
Qy 901 GCGTCAACGCGGCGCCGCAATGCGGCGGTAGGCTCAGCGCCAGCGGAGCGGCGGCTAG 960
Db |||||
Qy 901 GCGTCAACGCGGCGCCGCAATGCGGCGGTAGGCTCAGCGCCAGCGGAGCGGCGGCTAG 960
Db |||||
Qy 961 CGGTCCAGGTTCCGTTAGCGGATCCAGCTCTCAAGCGGAGGAGGAGCGGCGGTTTC 1020
Db |||||
Qy 961 CGGTCCAGGTTCCGTTAGCGGATCCAGCTCTCAAGCGGAGGAGGAGCGGCGGTTTC 1020
Db |||||
Qy 1021 TGGCGGAATGGCAGCGGCAACGGTTCTGATGATCTTCATGACCAATAGCTGTCCAGGGA 1080
Db |||||
Qy 1021 TGGCGGAATGGCAGCGGCAACGGTTCTGATGATCTTCATGACCAATAGCTGTCCAGGGA 1080
Db |||||
Qy 1081 TTTCTCGATCGAGCGCATCATAGAGCGGAGCGAGCGGAGACCCCAATGCGGCGATCG 1140
Db |||||
Qy 1081 TTTCTCGATCGAGCGCATCATAGAGCGGAGCGGAGCGGAGACCCCAATGCGGCGATCG 1140
Db |||||
Qy 1141 TGCACTGAGTTCCTGCGCGTTCCTATTCACAGTCCAGCGCGACTCAAGGGTGC 1200
Db |||||
Qy 1141 TGCACTGAGTTCCTGCGCGTTCCTATTCACAGTCCAGCGCGACTCAAGGGTGC 1200
Db |||||
Qy 1201 CGTGTGCGGCTGTGCCAAGTGTCAACAAACAGCTCTTCAGATGTCGGAATACGGCG 1260
Db |||||
Qy 1201 CGTGTGCGGCTGTGCCAAGTGTCAACAAACAGCTCTTCAGATGTCGGAATACGGCG 1260
Db |||||
Qy 1261 CATGATCCGACATTTTCCAGGTCGCGTGGACGACAGGTGATTTCTGTGAAAGCGCG 1320
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Db |||||
Qy 1321 TTGATCGAGTGTCTCATTTGCGAACGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1380
Db |||||
Qy 1321 TTGATCGAGTGTCTCATTTGCGAACGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1380
Db |||||
Qy 1381 CGGTGCGGCGGCGGCGGCGGCTGAGGACGATGGCTTTCGAGCGGACGATCAACC 1440
Db |||||
Qy 1381 CGGTGCGGCGGCGGCGGCGGCTGAGGACGATGGCTTTCGAGCGGACGATCAACC 1440
Db |||||
Qy 1441 GGGCTTTGAGCCCGCAGCAGCTGTTCTCAACAGAGCTTCTGTACCATCCGACAGTGC 1500
Db |||||
Qy 1441 GGGCTTTGAGCCCGCAGCAGCTGTTCTCAACAGAGCTTCTGTACCATCCGACAGTGC 1500
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Qy 1501 GATCAAGCGGCTGTGTCAGCCATCTTCGACCGCATATTTGTCGAGCTGAGTGAAGAT 1560
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Qy 1561 GAAGGCGTGAATCTCGACCGAGCGGCTGCTGCTTGAAGCCCATCATCTGTACAA 1620
Db |||||
Qy 1561 GAAGGCGTGAATCTCGACCGAGCGGCTGCTGCTTGAAGCCCATCATCTGTACAA 1620
Db |||||
Qy 1621 CCCGACATAGCGGCGATCAAGAGCGGCGGCGGAGATCGAGATGTGCCGAGAGAGTGA 1680
Db |||||
Qy 1621 CCCGACATAGCGGCGATCAAGAGCGGCGGCGGAGATCGAGATGTGCCGAGAGAGTGA 1680
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Qy 1681 CGCTTGTGAGCAGGACATGCGCGCTGGAACATTCGCGGCGGAGATGAGCGCTTGGCGCA 1740
Db |||||
Qy 1681 CGCTTGTGAGCAGGACATGCGCGCTGGAACATTCGCGGCGGAGATGAGCGCTTGGCGCA 1740
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Db |||||
Qy 1741 ACTGCTGCGCTGTGCGCGCTTTGCGATCCATGAGCTGAGTGCAGGATCACTGTT 1800
Db |||||
Qy 1801 CCTCTTCGCAATACAGCGACCGGCGCTGAGGAGCTCTTTCTCGAGCAGCTGAGGCG 1860
Db |||||
Qy 1801 CCTCTTCGCAATACAGCGACCGGCGCTGAGGAGCTCTTTCTCGAGCAGCTGAGGCG 1860
Db |||||
Qy 1861 GCGCGCGCAACCGCGCTGCGGATGAACCTGAGGTCCGAGCTCTAAAGTCTCCGC 1920
Db |||||

Db 1861 GCCGCCGCCACC CGCGCTGCGCATGAACTGGAGTAGGCTCCGACTCTAAAGTCTCCCC 1920
Qy 1921 CGTTCTCCATCCGAAAAATGTTTCATTGTGATGCGTTTGTGTCATTTCTCTCTCTAT 1980
Db 1921 CGTTCTCCATCCGAAAAATGTTTCATTGTGATGCGTTTGTGTCATTTCTCTCTCTAT 1980
Qy 1981 CCCTTATACCTACAAAAGCCCTTAATATTACGCAAAATGTGTATGTAATGTTTATTT 2040
Db 1981 CCCTTATACCTACAAAAGCCCTTAATATTACGCAAAATGTGTATGTAATGTTTATTT 2040
Qy 2041 TTTTATTTATACCTATATATTTATTTATTTATGATATGAAATGTTTCTTAAATCA 2100
Db 2041 TTTTATTTATACCTATATATTTATTTATTTATGATATGAAATGTTTCTTAAATCA 2100
Qy 2101 AGATTAGCCTCTCGAGCTTTATGTCCTCAGTAAACGAAAAACAAAATCCAAACTT 2160
Db 2101 AGATTAGCCTCTCGAGCTTTATGTCCTCAGTAAACGAAAAACAAAATCCAAACTT 2160
Qy 2161 GAAAGAACACAAAACACGAGAGAAATGCAACAAAGTAAAGTAAAGTTAA 2220
Db 2161 GAAAGAACACAAAACACGAGAGAAATGCAACAAAGTAAAGTAAAGTTAA 2220
Qy 2221 ACTAAGCTAAACGAGTAAAGTATTAATAAATACGGTTAAATTAATGATATGAT 2280
Db 2221 ACTAAGCTAAACGAGTAAAGTATTAATAAATACGGTTAAATTAATGATATGAT 2280
Qy 2281 CTACAGACGTATGTAACATACAAATTCAGCATTAATATATATGTCAGCGCGCATATC 2340
Db 2281 CTACAGACGTATGTAACATACAAATTCAGCATTAATATATATGTCAGCGCGCATATC 2340
Qy 2341 TCGGTGTCGCGCCCGTCTTAATCAATTTGTAATTTTAAACATAAATTTACCCAAA 2400
Db 2341 TCGGTGTCGCGCCCGTCTTAATCAATTTGTAATTTTAAACATAAATTTACCCAAA 2400
Qy 2401 ACGTTATCAATTTAGTATGCGAGATACAAAATCACCGACGAAACCAACAAATATCTA 2460
Db 2401 ACGTTATCAATTTAGTATGCGAGATACAAAATCACCGACGAAACCAACAAATATCTA 2460
Qy 2461 TGTATAAAAAATATAAATGTCATAACAA 2488
Db 2461 TGTATAAAAAATATAAATGTCATAACAA 2488

RESULT 2
ID AEB53800
XX AEB53800 standard; cDNA; 2488 BP.
AC AEB53800;
XX
DT 06-OCT-2005 (first entry)
XX
DE Drosophila nuclear receptor cDNA #14.
XX
KW Insecticide; pesticide; toxin; nuclear receptor; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO2005069859-A2.
XX
PD 04-AUG-2005.
XX
PF 13-JAN-2005; 2005WO-US001218.
XX
PR 13-JAN-2004; 2004US-0536337P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Thummel CS, King-Jones K, Horner M, Lam G;
XX
PI WPI; 2005-555376/56.
XX
DR P-P5DB; AEB53799.
XX
PT Composition useful for increasing effect of existing toxins to control

PT insects, and for inhibiting insect growth, comprises inhibitor of DHR96
PT activity, and optionally pesticide.
XX Disclosure; SEQ ID NO 28; 211pp; English.
XX
CC The invention relates to a composition comprising an inhibitor of DHR96
CC activity and optionally a pesticide. The invention also relates to an
CC insect comprising a gene, where the gene comprises a non-naturally
CC occurring mutation in the DHR96 gene, a method of enhancing the effect a
CC pesticide has on an insect involving administering to the insect an
CC inhibitor of DHR96 activity, a method of identifying an inhibitor of
CC DHR96 activity involving testing compounds for inhibition activity of
CC DHR96 and/or inhibition of xenobiotic activity and comparing the activity
CC of these compounds to known inhibitors of DHR96, a method of producing a
CC composition for inhibiting DHR96 activity involving admixing the
CC inhibitor with a pesticide and a composition produced by the method. The
CC composition and method are useful for enhancing the effect a pesticide
CC has on an insect, for identifying an inhibitor of DHR96 activity, for
CC identifying ligands for DHR96 and for producing a composition for
CC inhibiting DHR96 activity. The composition is useful for regulating
CC DHR96, preferably for inhibiting DHR96 gene expression or activity and
CC for increasing the effect of existing toxins or pesticides e.g., DDT to
CC control insects. The composition is useful for controlling insects e.g.,
CC silverfish, Dragonflies, Stoneflies, beetles, fleas, ants, bees, wasps,
CC termites etc. and decreases the resistance exhibited by the insects with
CC respect to toxins or pesticides. This sequence represents cDNA encoding a
CC Drosophila nuclear receptor used in the scope of the invention.
XX
SQ Sequence 2488 BP; 669 A; 669 C; 648 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2488; DB 14; Length 2488;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAATGTCAGCGGAAAAAAGGTATTTATTCATTAGTCAGAAAGTCTGGCATTTCTTGT 60
Db 1 AAAAAATGTCAGCGGAAAAAAGGTATTTATTCATTAGTCAGAAAGTCTGGCATTTCTTGT 60

Qy 61 TTTTGGTAAAGCGCAATTGTTGGAGGCGGAGCGAATAAAGTCGCTGCCATCGGC 120
Db 61 TTTTGGTAAAGCGCAATTGTTGGAGGCGGAGCGAATAAAGTCGCTGCCATCGGC 120

Qy 121 TCAAGATTATGTAAATGTCAGCAACGACCCCAACCAACGAACTGCAACTGCTCCACT 180
Db 121 TCAAGATTATGTAAATGTCAGCAACGACCCCAACCAACGAACTGCAACTGCTCCACT 180

Qy 181 TGGCCCAACGACCAATAGCGGACGGAACGACACCGTGGCGTTGGCAAGTGAACCCCA 240
Db 181 TGGCCCAACGACCAATAGCGGACGGAACGACACCGTGGCGTTGGCAAGTGAACCCCA 240

Qy 241 ACAGAGGCGGAAAGCGAGCCCAAGACACACACATACACAGAGAACGAGCAAGAG 300
Db 241 ACAGAGGCGGAAAGCGAGCCCAAGACACACACATACACAGAGAACGAGCAAGAG 300

Qy 301 AAACCGGTAGGCGAGGAGGCGCTGCCCCCAAGTTCCTCCAATATATACCAGCACCATCA 360
Db 301 AAACCGGTAGGCGAGGAGGCGCTGCCCCCAAGTTCCTCCAATATATACCAGCACCATCA 360

Qy 361 CAAGCCAGGATGGAACATCTCGACGAGCGCCAGCTTTGGCTGAGCCATCAAGA 420
Db 361 CAAGCCAGGATGGAACATCTCGACGAGCGCCAGCTTTGGCTGAGCCATCAAGA 420

Qy 421 GGAGGTCAAGCGGACATCTCGAGCTGAAACGACGAGCAACACAGCTTTTCCGCCAA 480
Db 421 GGAGGTCAAGCGGACATCTCGAGCTGAAACGACGAGCAACACAGCTTTTCCGCCAA 480

Qy 481 GGCCGAGAGTCCCGTGCCCTTCATGCGGCGCATGTGTCATGTCACGCTGCCCCGGTTC 540
Db 481 GGCCGAGAGTCCCGTGCCCTTCATGCGGCGCATGTGTCATGTCACGCTGCCCCGGTTC 540

Qy 541 CAACCTCCGCCAGCTCCAAACAAACAGCGCTGGAGATGCCAAATGGCGGAGGCCCA 600
Db 541 CAACCTCCGCCAGCTCCAAACAAACAGCGCTGGAGATGCCAAATGGCGGAGGCCCA 600

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QY 601 TTGSGCTGGAAGCTCTGCGCGCTGCACTCCAGCAGAGTATCCGCTAACCATCCGCT 660
Db 601 TTGSGCTGGAAGCTCTGCGCGCTGCACTCCAGCAGAGTATCCGCTAACCATCCGCT 660
QY 661 GAGCGGCAAGCAAGCACTCTCTCTCTATTTGCGGGATCGGGCAGTGGCAAGCACTACGG 720
Db 661 GAGCGGCAAGCAAGCACTCTCTCTCTATTTGCGGGATCGGGCAGTGGCAAGCACTACGG 720
QY 721 CGGTACAGCTGTGAGGGCTCGAAGGCTTCTTTAAAGCAAGTGGCAAGGATCTCAC 780
Db 721 CGGTACAGCTGTGAGGGCTCGAAGGCTTCTTTAAAGCAAGTGGCAAGGATCTCAC 780
QY 781 ATAGCGTTGCAAGGAGAACCCCACTGCATCATAGCAAGCGGAGAGAAACCGCTGCCA 840
Db 781 ATAGCGTTGCAAGGAGAACCCCACTGCATCATAGCAAGCGGAGAGAAACCGCTGCCA 840
QY 841 GTACTGCCGCTACCAAGAGTGCCTAACTCGGCGCATGAAGCGCAAGCGGTCCAGGAGGA 900
Db 841 GTACTGCCGCTACCAAGAGTGCCTAACTCGGCGCATGAAGCGCAAGCGGTCCAGGAGGA 900
QY 901 GCGTCAAGCGGCGCGCCCAATGCGGCGGGTAGGCTCAGGCCAGCGGAGCGCGAGTAG 960
Db 901 GCGTCAAGCGGCGCGCCCAATGCGGCGGGTAGGCTCAGGCCAGCGGAGCGCGAGTAG 960
QY 961 CGGTCCAGGTTCCGTAGGCGGATCCAGCTCTCAAGGCGGAGGAGGAGCGCGCTTC 1020
Db 961 CGGTCCAGGTTCCGTAGGCGGATCCAGCTCTCAAGGCGGAGGAGGAGGAGCGCGCTTC 1020
QY 1021 TGGCGGAATGGCGAGCGGCAACGGTTCCTGATGACTTCATGACCAATAGCGTGTCCAGGGA 1080
Db 1021 TGGCGGAATGGCGAGCGGCAACGGTTCCTGATGACTTCATGACCAATAGCGTGTCCAGGGA 1080
QY 1081 TTTCTCGATCAGCGGCATCATAGAGCGGAGCGAGCGGAGAGCCCAATCGCGCGATCG 1140
Db 1081 TTTCTCGATCAGCGGCATCATAGAGCGGAGCGAGCGGAGAGCCCAATCGCGCGATCG 1140
QY 1141 TGCACTGAGCTTCCTGCGGCTGGTCCCTATTTCCACAGTCCAGCGGACTACAAAGGGTGC 1200
Db 1141 TGCACTGAGCTTCCTGCGGCTGGTCCCTATTTCCACAGTCCAGCGGACTACAAAGGGTGC 1200
QY 1201 CGGTGCGGCCCTGTGCCAAGTGGTCAACAAACAGCTCTTCCAGATGGTCCGAATACGCGCG 1260
Db 1201 CGGTGCGGCCCTGTGCCAAGTGGTCAACAAACAGCTCTTCCAGATGGTCCGAATACGCGCG 1260
QY 1261 CATGATCGCGCACTTTTGCCAGGTGCCCTGGAAGCGAGTGTCTGCTGGAAGCGCG 1320
Db 1261 CATGATCGCGCACTTTTGCCAGGTGCCCTGGAAGCGAGTGTCTGCTGGAAGCGCG 1320
QY 1321 TTGGATCGAGCTGCTCATTTGCGAAGCGTGGCTGGTGCAGCATCGTTTCGCTGGATGACGG 1380
Db 1321 TTGGATCGAGCTGCTCATTTGCGAAGCGTGGCTGGTGCAGCATCGTTTCGCTGGATGACGG 1380
QY 1381 CGGTGCGCGCGCGGGCGGTGGACTAGGCCACGATGGCTCCTTTGAGCGACGATCAC 1440
Db 1381 CGGTGCGCGCGCGGGCGGTGGACTAGGCCACGATGGCTCCTTTGAGCGACGATCAC 1440
QY 1441 GGGCCTTCAGCCCAAGAGCTGTTCCTCAACAGAGCTTCTCGTACCATCGCAACAGTGC 1500
Db 1441 GGGCCTTCAGCCCAAGAGCTGTTCCTCAACAGAGCTTCTCGTACCATCGCAACAGTGC 1500
QY 1501 GATCAAGCGGTGTGTCAGCCATCTTCGACCGCATATTTGCGAGCTGAGTGAAGAT 1560
Db 1501 GATCAAGCGGTGTGTCAGCCATCTTCGACCGCATATTTGCGAGCTGAGTGAAGAT 1560
QY 1561 GAAAGCGGTGATCTCGACCGAGCGAGCTGTCTGCTTGAAGCCATCATATGTACAA 1620
Db 1561 GAAAGCGGTGATCTCGACCGAGCGAGCTGTCTGCTTGAAGCCATCATATGTACAA 1620
QY 1621 CCCGACATATCGCGGATCAAGAGCGGCGGAGATCGAGATGTCGCCGAGAGGTGTA 1680
Db 1621 CCCGACATATCGCGGATCAAGAGCGGCGGAGATCGAGATGTCGCCGAGAGGTGTA 1680
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QY 1681 CGTTGCTGAGAGCAGTGCAGCTGGAAACATCCGGGCGAGATGGAGCGCTTTGGCA 1740
Db 1681 CGTTGCTGAGAGCAGTGCAGCTGGAAACATCCGGGCGAGATGGAGCGCTTTGGCA 1740
QY 1741 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 CCTCTTCGCAATTAACAGCGACCGGCGCTGGAGGAGCTCTTCTCGAGCAGCTGGAGGC 1860
Db 1801 CCTCTTCGCAATTAACAGCGACCGGCGCTGGAGGAGCTCTTCTCGAGCAGCTGGAGGC 1860
QY 1861 GCGCGCGCCACCGGCGCTGGCGATGAACTGGAGTGGGTCCGACTCTAAAGTCTCCCC 1920
Db 1861 GCGCGCGCCACCGGCGCTGGCGATGAACTGGAGTGGGTCCGACTCTAAAGTCTCCCC 1920
QY 1921 CGTTCTCATTCGAAATAATGTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 CGTTCTCATTCGAAATAATGTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 CCTTTACCTTACAAAGCGCCCTAATATTAATGATATAGAAAATGTTTCTTAAATTT 2040
Db 1981 CCTTTACCTTACAAAGCGCCCTAATATTAATGATATAGAAAATGTTTCTTAAATTT 2040
QY 2041 TTTTATTTATTAACCTAATATTAATTAATGATATAGAAAATGTTTCTTAAAGTGA 2100
Db 2041 TTTTATTTATTAACCTAATATTAATTAATGATATAGAAAATGTTTCTTAAAGTGA 2100
QY 2101 AGATTAGCTCTCGAGCTTTATGTCAGTAAACGAAACAAACAAATCCAAACTT 2160
Db 2101 AGATTAGCTCTCGAGCTTTATGTCAGTAAACGAAACAAACAAATCCAAACTT 2160
QY 2161 GAAAGAACACAAACACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTAA 2220
Db 2161 GAAAGAACACAAACACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTAA 2220
QY 2221 ACTAAAGCTAAACGAGTAAAGATATTAATAAATACCGTTAAATTAATGATATGAT 2280
Db 2221 ACTAAAGCTAAACGAGTAAAGATATTAATAAATACCGTTAAATTAATGATATGAT 2280
QY 2281 CTACAGAGTATGTAAACATACAAATTCAGATATAATATATATGTCAGCGGCGCATATC 2340
Db 2281 CTACAGAGTATGTAAACATACAAATTCAGATATAATATATATGTCAGCGGCGCATATC 2340
QY 2341 TGCGGTGCTGCGCGCTTCTTAAATCAATTTGATTTACTTTTAAACATAAAATTTTACC 2400
Db 2341 TGCGGTGCTGCGCGCTTCTTAAATCAATTTGATTTACTTTTAAACATAAAATTTTACC 2400
QY 2401 ACGTTATCAATTAAGTACGAGATACAAATAATCACCGAGCAAAATCATATACTATA 2460
Db 2401 ACGTTATCAATTAAGTACGAGATACAAATAATCACCGAGCAAAATCATATACTATA 2460
QY 2461 TGTATAAAATAATAAACTGCAATAACAA 2488
Db 2461 TGTATAAAATAATAAACTGCAATAACAA 2488
RESULT 3
ABL07558/c
ID ABL07558 standard; cdna; 4483 BP.
XX
AC ABL07558;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17156.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
OS pharmaceutical; gene; ss.
XX
PN Drosophila melanogaster.
WO200171042-A2.
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QY 481 GCGCGAGGTCCTGCGGCCCTTCATGACGAGCCATGTCTCCATGGTCCAGGTGCTGCGCGGCTC 540
Db 16309 GCGCGAGGTCCTGCGGCCCTTCATGACGAGCCATGTCTCCATGGTCCAGGTGCTGCGCGGCTC 16250

QY 541 CAACTCGCGCAGCTCAACAAACAAACAGCGCTGGAGATGCCAAATGCGCGAGGCGCCAA 600
Db 16249 CAACTCGCGCAGCTCAACAAACAAACAGCGCTGGAGATGCCAAATGCGCGAGGCGCCAA 16190

QY 601 TTCGGCTGGAGGCTCTGCGCGCCGCTGACGTCCAGACGACGATATCCGCTCAACCATCCGCT 660
Db 16189 TTCGGCTGGAGGCTCTGCGCGCCGCTGACGTCCAGACGACGATATCCGCTCAACCATCCGCT 16130

QY 661 GAGCGCGAGGACCACTCTGCTCTATTTGCGGGGATCGGGCCAGTGGCAAGCACTACCG 720
Db 16129 GAGCGCGAGGACCACTCTGCTCTATTTGCGGGGATCGGGCCAGTGGCAAGCACTACCG 16070

QY 721 CGGTACAGCTGTGAGGCTGCAAGGCTTCTTTAAACGACAGTGGCGGACGATCTCAC 780
Db 16069 CGGTACAGCTGTGAGGCTGCAAGGCTTCTTTAAACGACAGTGGCGGACGATCTCAC 16010

QY 781 ATACGCTTCGAGGGAACCGAACTGACATCATAGACAAAGCGGACAGGAAACGCTGCGCA 840
Db 16009 ATACGCTTCGAGGGAACCGAACTGACATCATAGACAAAGCGGACAGGAAACGCTGCGCA 15950

QY 841 GTACTGCCGCTACCAAGATGCCCTAACCTGCGGCATGAAGCGGAGCGGTCCAGGAGCA 900
Db 15949 GTACTGCCGCTACCAAGATGCCCTAACCTGCGGCATGAAGCGGAGCGGTCCAGGAGCA 15890

QY 901 GGGTCMAACGGCGCCGCGCAATGCGCGGGTAGGCTCAGCGCCAGCGAGGCGGCAAGTAG 960
Db 15889 GGGTCMAACGGCGCCGCGCAATGCGCGGGTAGGCTCAGCGCCAGCGAGGCGGCAAGTAG 15830

QY 961 CGGTCCAGGCTCGGTAGGCGGATCCAGCTCTCAAGCGGAGGAGGAGGCGGCTTTC 1020
Db 15829 CGGTCCAGGCTCGGTAGGCGGATCCAGCTCTCAAGCGGAGGAGGAGGCGGCTTTC 15770

QY 1021 TGGCGGAATGGGCGAGCGGCAACGGTTCTGATGACTTCATGACCAATAGCGGTCCAGGGA 1080
Db 15769 TGGCGGAATGGGCGAGCGGCAACGGTTCTGATGACTTCATGACCAATAGCGGTCCAGGGA 15710

QY 1081 TTTCTCGATCGAGCGCATCATAGAGCCGAGCAGCGAGCGGAGACCCAAATGCGGCGATCG 1140
Db 15709 TTTCTCGATCGAGCGCATCATAGAGCCGAGCAGCGAGCGGAGACCCAAATGCGGCGATCG 15650

QY 1141 TGCACCTGAGCTTCCTGCGGTTGCTCCCTATTTCCACAGTCCAGCGGACTACAAGGTGC 1200
Db 15649 TGCACCTGAGCTTCCTGCGGTTGCTCCCTATTTCCACAGTCCAGCGGACTACAAGGTGC 15590

QY 1201 CGTGTGCGGCCCTGTGCCAAGTGGTCAACAAACAGCTCTTCCAGATGGTCCGAATAGCGCG 1260
Db 15589 CGTGTGCGGCCCTGTGCCAAGTGGTCAACAAACAGCTCTTCCAGATGGTCCGAATAGCGCG 15530

QY 1261 CATGATGCGCGCATTTGCGCCAGTGGCGTGAACGACAGGTGATTTCTGCTGAAAGCGCG 1320
Db 15529 CATGATGCGCGCATTTGCGCCAGTGGCGTGAACGACAGGTGATTTCTGCTGAAAGCGCG 15470

QY 1321 TTGGATCGAGCTGCTCATTTGCGAAGCTGGCCCTGGTGCAGCATCGTTTTCGCTGGATGACGG 1380
Db 15469 TTGGATCGAGCTGCTCATTTGCGAAGCTGGCCCTGGTGCAGCATCGTTTTCGCTGGATGACGG 15410

QY 1381 CGGTGCGCGCGCGGCGGTGGACTAGGCCACGATGGCTCTTTGAGCGGACGATCACCC 1440
Db 15409 CGGTGCGCGCGCGGCGGTGGACTAGGCCACGATGGCTCTTTGAGCGGACGATCACCC 15350

QY 1441 GGGCCCTTACGCCCCAGCAGCTGTTCCTCAACAGAGCTTTCGTACCATCGCAACAGTGC 1500
Db 15349 GGGCCCTTACGCCCCAGCAGCTGTTCCTCAACAGAGCTTTCGTACCATCGCAACAGTGC 15290

QY 1501 GATCAAGCCGCTGTGTAGCCATCTTCGACCGCATATTTGTGCGAGCTGAGGTAAAGAT 1560
Db 15289 GATCAAGCCGCTGTGTAGCCATCTTCGACCGCATATTTGTGCGAGCTGAGGTAAAGAT 15230
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QY 1561 GAAGCGGCTGAATCTCGAACCGACGCGAGCTGTCTGCTTGAAGGCCATCATACTGTACAA 1620
Db 15229 GAAGCGGCTGAATCTCGAACCGACGCGAGCTGTCTGCTTGAAGGCCATCATACTGTACAA 15170

QY 1621 CCGGACATACCGGGGATCAAGACCGGGCGGAGATCGAGATGTGCGCGGAGAGGTGA 1680
Db 15169 CCGGACATACCGGGGATCAAGACCGGGCGGAGATCGAGATGTGCGCGGAGAGGTGA 15110

QY 1681 CGCTTTGCTGAGACGACGCTCGGCTGGAAACATCCGGGCGACGATGAGCGCTTTCGCGCA 1740
Db 15109 CGCTTTGCTGAGACGACGCTCGGCTGGAAACATCCGGGCGACGATGAGCGCTTTCGCGCA 15050

QY 1741 ACTGCTGCTGCTGTCTGCGCGCTTTGCGATCGATCGACCTGGAAGTGCAGGATCACTGTT 1800
Db 15049 ACTGCTGCTGCTGTCTGCGCGCTTTGCGATCGATCGACCTGGAAGTGCAGGATCACTGTT 14990

QY 1801 CCTCTTCGCGCATTACAGGACCGCGCTGGAGAGCTCTTTCTCGAGCAGCTGGAGGC 1860
Db 14989 CCTCTTCGCGCATTACAGGACCGCGCTGGAGAGCTCTTTCTCGAGCAGCTGGAGGC 14930

QY 1861 GCGCGCGCCACCGCGCTGGCGATGAAACTGAGTAGGTCGCCGACTCTAAAAGTCTCCCC 1920
Db 14929 GCGCGCGCCACCGCGCTGGCGATGAAACTGAGTAGGTCGCCGACTCTAAAAGTCTCCCC 14870

QY 1921 CGTTCTCCATCCGAAAAATGTTTCATTGTGATTGCGTTTGTGTCATTTCTCTCTAT 1980
Db 14869 CGTTCTCCATCCGAAAAATGTTTCATTGTGATTGCGTTTGTGTCATTTCTCTCTAT 14810

QY 1981 CCTTATACCTTACAAAAAGCCCCCTAATATTAACGAAAAATGTGATGTGTAATTTT 2040
Db 14809 CCTTATACCTTACAAAAAGCCCCCTAATATTAACGAAAAATGTGATGTGTAATTTT 14750

QY 2041 TTTTATTTTATTAACCTAATATTAATTTATTTGATATAGAAATGTTTTCTTAAGATGA 2100
Db 14749 TTTTATTTTATTAACCTAATATTAATTTATTTGATATAGAAATGTTTTCTTAAGATGA 14690

QY 2101 AGATTAGGCTCTCTGACGTTTATGTCCAGTAAACGAAAAACAAACAAAAATCCAAAATCT 2160
Db 14689 AGATTAGGCTCTCTGACGTTTATGTCCAGTAAACGAAAAACAAACAAAAATCCAAAATCT 14630

QY 2161 GAAAAAGAACAAAAACAGAACGAGAAAAATGACACAAGCAAAAGTAAAGTAAAAAGTTAA 2220
Db 14629 GAAAAAGAACAAAAACAGAACGAGAAAAATGACACAAGCAAAAGTAAAGTAAAAAGTTAA 14570

QY 2221 ACTAAAGCTTAAACGAGTAGTAAGATATTAATAAATGTTTAAATTAATGATAGTTATGAT 2280
Db 14569 ACTAAAGCTTAAACGAGTAGTAAGATATTAATAAATGTTTAAATTAATGATAGTTATGAT 14510

QY 2281 CTACAGAGCTATGTAAACATACAAATTCAGCATAAATATATATGTGACGAGCGCATATC 2340
Db 14509 CTACAGAGCTATGTAAACATACAAATTCAGCATAAATATATATGTGACGAGCGCATATC 14450

QY 2341 TCGCGTGTGCGCCCGTTCTAAATCAATGTGTAATTTCTTTTAAACATTAATTTTACCCAAA 2400
Db 14449 TCGCGTGTGCGCCCGTTCTAAATCAATGTGTAATTTCTTTTAAACATTAATTTTACCCAAA 14390

QY 2401 ACGTTTCAATTTAGTGTGAGATACAAAAATCAACGAGAAAAACCAACAAATATATCTA 2460
Db 14389 ACGTTTCAATTTAGTGTGAGATACAAAAATCAACGAGAAAAACCAACAAATATATCTA 14330

QY 2461 TGTATAAAAAATATAAACTGCATACAA 2488
Db 14329 TGTATAAAAAATATAAACTGCATACAA 14302
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RESULT 5

ABL07530/c

ID ABL07530 standard; cDNA; 18737 BP.

XX

AC ABL07530;

XX

DT 26-MAR-2002 (first entry)

XX

Drosophila melanogaster expressed polynucleotide SEQ ID NO 17072.
Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
Drosophila melanogaster.
WO200171042-A2.
27-SEP-2001.
23-MAR-2001; 2001WO-US009231.
23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
(PBEK) PE CORP NY.
Venter JC, Adams M, Li PWD, Myers EW;
WPI; 2001-656860/75.
P-PSDB; ABB63427.
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
interactions.
Claim 1; SEQ ID NO 17072; 2lpp + Sequence Listing; English.
The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
ABBS72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 18737 BP; 4743 A; 4303 C; 4508 G; 5183 T; 0 U; 0 Other;
Query Match 100.0%; Score 2488; DB 4; Length 18737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAAAAATGTCGACGCGGAAAAAGGTAATTTATTCATTAGTCAGAAAAGTCGGCAATCTTTGT 60
Db 16789 AAAAAATGTCGACGCGGAAAAAGGTAATTTATTCATTAGTCAGAAAAGTCGGCAATCTTTGT 16730
Qy 61 TTGTTGGTAAAGGCGCAATTTGTTGGAGGCGGAGGCAATTAAGTCGCTGCCATCGGC 120
Db 16729 TTGTTGGTAAAGGCGCAATTTGTTGGAGGCGGAGGCAATTAAGTCGCTGCCATCGGC 16670
Qy 121 TCAAGATTATGTAATGACGACCAACGACCCACCAACGAACTGCAACCTGCTCCACT 180
Db 16669 TCAAGATTATGTAATGACGACCAACGACCCACCAACGAACTGCAACCTGCTCCACT 16610
Qy 181 TGGCCCAACGCAATAGCGGACGCGACGACGCTGCGCTGGCAAAAGTGAACCCCA 240
Db 16609 TGGCCCAACGCAATAGCGGACGCGACGACGCTGCGCTGGCAAAAGTGAACCCCA 16550
Qy 241 ACAGAGCGCGAAGCGGACCCAGACACCAATACACACGAGAGAACGAGCAAGAG 300
Db 16549 ACAGAGCGCGAAGCGGACCCAGACACCAATACACACGAGAGAACGAGCAAGAG 16490
Qy 301 AAACCGGTAGCGGAGGAGGCGCTGCCCCAGTTCCTCAATATATACCAGACCAATCA 360
Db 16489 AAACCGGTAGCGGAGGAGGCGCTGCCCCAGTTCCTCAATATATACCAGACCAATCA 16430
Qy 361 CAAGCCCAAGGATGGCAACTGCGACACGACGACGCTTTTGGCTGAGCCCAATCAAGGA 420
Db 16429 CAAGCCCAAGGATGGCAACTGCGACACGACGACGCTTTTGGCTGAGCCCAATCAAGGA 16370

Qy 421 GGAGGTCAAGCGGACATCTCGCAGCTGAACGACAGCAACACAGCAGCTTTTCGCCCAA 480
Db 16369 GGAGGTCAAGCGGACATCTCGCAGCTGAACGACAGCAACACAGCAGCTTTTCGCCCAA 16310
Qy 481 GGCCGAGAGTCCCGTCCCTTCATCAGGCGCATGTCCATGGTCCAGTGTGCGCGGCTC 540
Db 16309 GGCCGAGAGTCCCGTCCCTTCATCAGGCGCATGTCCATGGTCCAGTGTGCGCGGCTC 16250
Qy 541 CAACTCCGCGAGCTCCAAACAAACAGCGCTGGAGATGCCAAATGGCGGAGGCCCAA 600
Db 16249 CAACTCCGCGAGCTCCAAACAAACAGCGCTGGAGATGCCAAATGGCGGAGGCCCAA 16190
Qy 601 TTGCGCTGAGAGGCTCTGCGCGCGCTGCAGTCCAGCAGCATATCCCGCTAAACATCCGCT 660
Db 16189 TTGCGCTGAGAGGCTCTGCGCGCGCTGCAGTCCAGCAGCATATCCCGCTAAACATCCGCT 16130
Qy 661 GAGCGGACGACACCTCTGCTCTATTTTCGGGGATTCGGGCGAGTGGCAAGCACTACGG 720
Db 16129 GAGCGGACGACACCTCTGCTCTATTTTCGGGGATTCGGGCGAGTGGCAAGCACTACGG 16070
Qy 721 CGTGTACAGCTGTGAGGCTGCAAGGCTTCTTTAAACGACAGTGGCGAGGATCTCAC 780
Db 16069 CGTGTACAGCTGTGAGGCTGCAAGGCTTCTTTAAACGACAGTGGCGAGGATCTCAC 16010
Qy 781 ATACGCTTGCAGGAGAAACCGCAACTGCATATAGCAAGCGGACAGAGAACCGCTGCCA 840
Db 16009 ATACGCTTGCAGGAGAAACCGCAACTGCATATAGCAAGCGGACAGAGAACCGCTGCCA 15950
Qy 841 GTACTGCGGTACAGAGTGCCTAACCTCGCGCATGAAGCGGAGCGGTTCACGAGGA 900
Db 15949 GTACTGCGGTACAGAGTGCCTAACCTCGCGCATGAAGCGGAGCGGTTCACGAGGA 15890
Qy 901 GCGTCAAGCGGCGCGCGCAATGCGCGGCTAGGCTCAGCGCGGAGCGGCGGCTAG 960
Db 15889 GCGTCAAGCGGCGCGCGCAATGCGCGGCTAGGCTCAGCGCGGAGCGGCGGCTAG 15830
Qy 961 CCGTCCAGGTTCCGTAGCGGATCCAGTCTCAAGCGGAGGAGGAGCGGCGGCTTTC 1020
Db 15829 CCGTCCAGGTTCCGTAGCGGATCCAGTCTCAAGCGGAGGAGGAGCGGCGGCTTTC 15770
Qy 1021 TGGCGGAATGGCAGCGGCAACCGTTCTGATGACTTCATGACCAATAGCTGTCCAGGA 1080
Db 15769 TGGCGGAATGGCAGCGGCAACCGTTCTGATGACTTCATGACCAATAGCTGTCCAGGA 15710
Qy 1081 TTTCTCGATCAGCGGCAATAGAGCGCGAGCGGAGCGGAGACCAATGCGGCGATCG 1140
Db 15709 TTTCTCGATCAGCGGCAATAGAGCGCGAGCGGAGCGGAGACCAATGCGGCGATCG 15650
Qy 1141 TGCATCAGCTTCTCGCGCTTGGTCCCTATTCCACAGTCCAGCGGACTACAAAGGCTGC 1200
Db 15649 TGCATCAGCTTCTCGCGCTTGGTCCCTATTCCACAGTCCAGCGGACTACAAAGGCTGC 15590
Qy 1201 CGTGTGCGGCGCTGTGCGCAAGTGGTCAAACAAACAGCTCTTCCAGATGTGCAATACGCG 1260
Db 15589 CGTGTGCGGCGCTGTGCGCAAGTGGTCAAACAAACAGCTCTTCCAGATGTGCAATACGCG 15530
Qy 1261 CATGATCGCGCATTTTCCCGAGGTCGCTGGACGACAGGTCGATCTGCTGGAAGCGC 1320
Db 15529 CATGATCGCGCATTTTCCCGAGGTCGCTGGACGACAGGTCGATCTGCTGGAAGCGC 15470
Qy 1321 TTGGATCAGCTGCTCAATTCGAAACGTGGCTGGTGGAGATCGTTCGCTGGATGACGG 1380
Db 15469 TTGGATCAGCTGCTCAATTCGAAACGTGGCTGGTGGAGATCGTTCGCTGGATGACGG 15410
Qy 1381 CGGTGCGGCGGCGGCGGCTGGACTAGGCAAGTGGCTCTTTGAGCGACGATCAC 1440
Db 15409 CGGTGCGGCGGCGGCGGCTGGACTAGGCAAGTGGCTCTTTGAGCGACGATCAC 15350
Qy 1441 GGGCTTTACGCGCGGAGGCTGTTCCCAACGAGGCTCTCGTACCATCGCAACAGTC 1500
Db 15349 GGGCTTTACGCGCGGAGGCTGTTCCCAACGAGGCTCTCGTACCATCGCAACAGTC 15290


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RESULT 7
AAQ14176
ID AAQ14176 standard; cDNA; 2304 BP.
XX
AC AAQ14176;
XX
XX 25-MAR-2003 (revised)
DT 07-JAN-1992 (first entry)
XX
DE Clone pXR2C8 encoding insect steroid receptor XR2C.
XX
XX fruit fly; ultraspiracle locus; USP; transcription regulation; ss.
XX
OS Drosophila melanogaster.
XX
XX Key Location/Qualifiers
FH 163..1704
FT CDS
FT /*tag= a
FT /*product= "XR2C"
XX
XX WO9114695-A.
XX
XX 03-OCT-1991..
XX
XX 22-MAR-1990; . 90US-00497935.
XX
XX 22-MAR-1990; . 90US-00497935.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Oro AE, Evans RM;
XX
XX WPI; 1991-310528/42.
DR P-PSDB; AAR14304.
XX
XX New insect receptor polypeptide(s) activated by retinoic acid - for
PT identification of compounds able to affect gene transcription.
XX
XX Claim 3; Fig.1; 32pp; English.
XX
XX A Southern blot of D.melanogaster EcoRI-digested, genomic DNA was
XX screened with a probe comprising the DNA-binding domain of hRAR- alpha-
XX encoding DNA. Potential homologs of vertebrate steroid hormone receptors
XX were identified. One group mapped to 2C9 on the D. melanogaster first
XX chromosome and was labelled XR2C. A portion of a genomic insert
XX hybridising most strongly to the fragment of the hRAR- alpha-encoding DNA
XX probe was sequenced. The amino acid sequence deduced from it resembled a
XX steroid receptor DNA binding domain. The insert was used to screen a
XX total third instar larval imaginal disc cDNA library. The longest
XX positive clone was pXR2C8 and has the sequence given here. (Updated on 25
XX -MAR-2003 to correct PA field.)
XX
XX Sequence 2304 BP; 631 A; 619 C; 603 G; 451 T; 0 U; 0 Other;
XX
XX Query Match 90.0%; Score 2238.2; DB 2; Length 2304;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 2269; Conservative 0; Mismatches 3; Indels 9; Gaps 2;
XX
XX 209 GGACACGGTGGCGTTGGCAAGTGAACCCCAACAGAGAGGCGAAGCGAGCAC 268
XX 1 GGACACGGTGGCGTTGGCAAGTGAACCCCAACAGAGAGGCGAAGCGAGCAC 60
XX
XX 269 ACCACATACACAGAAAGAGACGACAGAAACCGGTAGGCGGAGGCGCGTGC 328
XX 61 ACCACATACACAGAAAGAGACGACAGAAACCGGTAGGCGGAGGCGCGTGC 120
XX
XX 329 CCAAGTTCCTCAATATACCCAGCACCATCAACAGCCGAGGATGGAACAAC 388
XX 121 CCAAGTTCCTCAATATACCCAGCACCATCAACAGCCGAGGATGGAACAAC 180
XX
XX 389 GACGCCAGCTTCGCTGAGCCACATCAAGAGGAGGTCAAGCCGGACATCTCG 448
XX 181 GACGCCAGCTTCGCTGAGCCACATCAAGAGGAGGTCAAGCCGGACATCTCG 240
XX
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QY 449 AACGACAGCAACACAGCAGCTTTTCGCCCAAGGCCGAGAGTCCCGTGCCTTCATGCAG 508
DB 241 AACGACAGCAACACAGCAGCTTTTCGCCCAAGGCCGAGAGTCCCGTGCCTTCATGCAG 300
QY 509 GCCATGTCATGGTCCACAGTGTCCCGCGCTCCAACTCCGCCAGCTCCAAACAAACAGC 568
DB 301 GCCATGTCATGGTCCACAGTGTCCCGCGCTCCAACTCCGCCAGCTCCAAACAAACAGC 360
QY 569 GCTGGAGATGCCCAATGCGCAGCGCCCAATTCGGCTGGAGGCTCTGCGCGCGCTGCA 628
DB 361 GCTGGAGATGCCCAATGCGCAGCGCCCAATTCGGCTGGAGGCTCTGCGCGCGCTGCA 420
QY 629 GTCCAGCAGCAGTATCCGCCTAAACCATCCGCTAGCGGCAGCAACACACTCTGCTCTATT 688
DB 421 GTCCAGCAGCAGTATCCGCCTAAACCATCCGCTAGCGGCAGCAACACACTCTGCTCTATT 480
QY 689 TCGCGGAGATCGGCGCAGTGGCAAGCACTACCGCGTGTACAGTGTGAGGGGTGCAAGGCG 748
DB 481 TCGCGGAGATCGGCGCAGTGGCAAGCACTACCGCGTGTACAGTGTGAGGGGTGCAAGGCG 540
QY 749 TTCTTTAAACGACAGTGGCGAAGGATCTCACATACGCTTCGAGGGAGAACCGCAACTGC 808
DB 541 TTCTTTAAACGACAGTGGCGAAGGATCTCACATACGCTTCGAGGGAGAACCGCAACTGC 600
QY 809 ATCATAGACAAAGCGCAGAGGAACCGCTGCCAGTACTGCCGTACAGAGTGCCTTAACC 868
DB 601 ATCATAGACAAAGCGCAGAGGAACCGCTGCCAGTACTGCCGTACAGAGTGCCTTAACC 660
QY 869 TCGGCGATGAAGCGCGAAGCGGTCCAGAGAGCGGTCAACCGCGCGCCGCAATCGGCG 928
DB 661 TCGGCGATGAAGCGCGAAGCGGTCCAGAGAGCGGTCAACCGCGCGCCGCAATCGGCG 720
QY 929 GGTAGGCTCAGCGCCAGCGGAGGCGGAGTCCAGGTCCAGGTTCGGTAGGCGGATCCAGC 988
DB 721 GGTAGGCTCAGCGCCAGCGGAGGCGGAGTCCAGGTTCGGTAGGCGGATCCAGC 780
QY 989 TCTCAAGCGGAGGAGGAGGCGGCGTTTCTCGCGGAATGGGCGAGCGGCAACCGTTCT 1048
DB 781 TCTCAAGCGGAGGAGGAGGCGGCGTTTCTCGCGGAATGGGCGAGCGGCAACCGTTCT 840
QY 1049 GATGACTTTCATGACCAATAGCGTGTCCAGGATTTCTCGATCGAGCGCATCATAGAGCC 1108
DB 841 GATGACTTTCATGACCAATAGCGTGTCCAGGATTTCTCGATCGAGCGCATCATAGAGCC 900
QY 1109 GAGCAGCAGCGGAGACCCCAATGCGGATCGTGCATGACGTTCTCTGCGGTTGGTCCC 1168
DB 901 GAGCAGCAGCGGAGACCCCAATGCGGATCGTGCATGACGTTCTCTGCGGTTGGTCCC 960
QY 1169 TATTCCACAGTCCAGCGCGGACTACAGGGTCCCGTGTGCGGCCCTGTGCAAGTGGTCAAC 1228
DB 961 TATTCCACAGTCCAGCGCGGACTACAGGGTCCCGTGTGCGGCCCTGTGCAAGTGGTCAAC 1020
QY 1229 AAAACAGCTCTTCCAGATGGTTCGAATACCGCGCAGATGATGCGCATCTTTGCCAGGTGCG 1288
DB 1021 AAAACAGCTCTTCCAGATGGTTCGAATACCGCGCAGATGATGCGCATCTTTGCCAGGTGCG 1080
QY 1289 CTGGACGACCAAGTGTCTGCTCAAAAGCCGCTTGGATCGAGCTGCTCATTTGCCAAGCTG 1348
DB 1081 CTGGACGACCAAGTGTCTGCTCAAAAGCCGCTTGGATCGAGTCTGCTCATTTGCCAAGCTG 1140
QY 1349 GCCTGGTGCAGATCTGCTGATGACGGCGGTGCGCGCGCGGGGGGGGGTGGACTA 1408
DB 1141 GCCTGGTGCAGATCTGCTGATGATGACGGCGGTGCGCGCGCGGGGGGGGGTGGACTA 1200
QY 1409 GGCCACAGATGCTCTTTTGAAGCGACGATCAACCGGCGCTTTCAGCCCCCAGCAGCTGTTCCTC 1468
DB 1201 GGCCACAGATGCTCTTTTGAAGCGACGATCAACCGGCGCTTTCAGCCCCCAGCAGCTGTTCCTC 1260
QY 1469 AACGACAGCTTCTGTTACCATCGCAACAGTGGGATCAAGCGGCTGTGTGAGCCATCTTC 1528
DB 1261 AACGACAGCTTCTGTTACCATCGCAACAGTGGGATCAAGCGGCTGTGTGAGCCATCTTC 1320
```


Db 121 CAGTTCTCCAAATATATACCGAGCACCAATCACAGCCAGGATGAGCAACTGCGACCAG 180
Qy 389 GAGCCAGCTTTTCGGCTGAGCCACATCAAGAGGAGGTCAAGCCGACATCTCGCAGCTG 448
Db 181 GAGCCAGCTTTTCGGCTGAGCCACATCAAGAGGAGGTCAAGCCGACATCTCGCAGCTG 240
Qy 449 AACGACAGCAACAAAGCAGCTTTTCGCCAAGGCCGAGAGTCCCGTGCCCTTCATGCAAG 508
Db 241 AACGACAGCAACAAAGCAGCTTTTCGCCAAGGCCGAGAGTCCCGTGCCCTTCATGCAAG 300
Qy 509 GCCATGTCATGTCACAGTGTCCCGGCTCCAACTCCGCGCAGCTTCCAAACAAACAGC 568
Db 301 GCCATGTCATGTCACAGTGTCCCGGCTCCAACTCCGCGCAGCTTCCAAACAAACAGC 360
Qy 569 GCTGGAGATGCCAAATGGCGAGCGGCCAAATTCGGCTGAGGCTCTCGCGCGCTGCA 628
Db 361 GCTGGAGATGCCAAATGGCGAGCGGCCAAATTCGGCTGAGGCTCTCGCGCGCTGCA 420
Qy 629 GTCCAGCAGATATCCGCTTAACATCCGCTGAGCGGAGCAAGCACTCTGCTCTATT 688
Db 421 GTCCAGCAGATATCCGCTTAACATCCGCTGAGCGGAGCAAGCACTCTGCTCTATT 480
Qy 689 TCGGGGATCGGSCCAGTGCAGCACTACGGGTGTACAGCTGTGAGGGCTGCAAGGCG 748
Db 481 TCGGGGATCGGSCCAGTGCAGCACTACGGGTGTACAGCTGTGAGGGCTGCAAGGCG 540
Qy 749 TTCTTTAAACGACAGTGCAGGATCTCACATACGCTTGAGGGAGAACCGCACTGC 808
Db 541 TTCTTTAAACGACAGTGCAGGATCTCACATACGCTTGAGGGAGAACCGCACTGC 600
Qy 809 ATCATAGACAAGCGGAGAGAAACCGCTGCCAGTACTGCCGTACAGAAAGTGCCTAAC 868
Db 601 ATCATAGACAAGCGGAGAGAAACCGCTGCCAGTACTGCCGTACAGAAAGTGCCTAAC 660
Qy 869 TCGGCGATGAAGCGGAGCGGTCCAGAGAGCGTCAACGGCGCCGCGCAATGGGCG 928
Db 661 TCGGCGATGAAGCGGAGCGGTCCAGAGAGCGTCAACGGCGCCGCGCAATGGGCG 720
Qy 929 GGTAGGCTCAGCGCAGCGAGCGCGCAGTAGCGGTCCAGGTTCCGTTAGCGGATCCAGC 988
Db 721 GGTAGGCTCAGCGCAGCGAGCGCGCAGTAGCGGTCCAGGTTCCGTTAGCGGATCCAGC 780
Qy 989 TCTCAAGCGGAGGAGGAGCGCGGTTCTGCGGGAATGGGAGCGGCAACGCTTCT 1048
Db 781 TCTCAAGCGGAGGAGGAGCGCGGTTCTGCGGGAATGGGAGCGGCAACGCTTCT 840
Qy 1049 GATGACTTCATGACCAATAGCTGTCCAGGATTTCTCGATCGAGGCAATCATAGAGCC 1108
Db 841 GATGACTTCATGACCAATAGCTGTCCAGGATTTCTCGATCGAGGCAATCATAGAGCC 900
Qy 1109 GAGCAGCAGCGAGACCCAAATGCGCGCATCTGCACTGACGTTCTGCGCGTTGCTGCC 1168
Db 901 GAGCAGCAGCGAGACCCAAATGCGCGCATCTGCACTGACGTTCTGCGCGTTGCTGCC 960
Qy 1169 TATTCACAGTCCAGCGGACTACAAGGTTGCGGTGCGGCCCTGTGCCAAGTGGTCAAC 1228
Db 961 TATTCACAGTCCAGCGGACTACAAGGTTGCGGTGCGGCCCTGTGCCAAGTGGTCAAC 1020
Qy 1229 AAGCAGCTTCCAGATGTCGAATACGCGCGCATGATGCCGCACTTTGCCCGCAGTGGCG 1288
Db 1021 AAGCAGCTTCCAGATGTCGAATACGCGCGCATGATGCCGCACTTTGCCCGCAGTGGCG 1080
Qy 1289 CTGGACGACAGGTGATCTGCTGAAAGCGGCTTGGATCGAGCTGCTCATTCGGAACGTG 1348
Db 1081 CTGGACGACAGGTGATCTGCTGAAAGCGGCTTGGATCGAGCTGCTCATTCGGAACGTG 1140
Qy 1349 GCTGGTGCAGATGCTTTGCTGGATGACGGCGGTGCGCGGCGGGGCGGTGGACTA 1408
Db 1141 GCTGGTGCAGATGCTTTGCTGGATGACGGCGGTGCGCGGCGGGGCGGTGGACTA 1200
Qy 1409 GSCCAGATGGCTCTTTGAGCGACGATCACGGGCGCTTCAGCGCCAGCAGCTGTTCCTC 1468
Db 1201 GSCCAGATGGCTCTTTGAGCGACGATCACGGGCGCTTCAGCGCCAGCAGCTGTTCCTC 1260

Qy 1469 AACCAGAGCTTCTCGTACCATCGCAACAGTGGGATCAAAAGCCGGTGTGTGAGCCATCTTC 1528
Db 1261 AACCAGAGCTTCTCGTACCATCGCAACAGTGGGATCAAAAGCCGGTGTGTGAGCCATCTTC 1320
Qy 1529 GACCGCATATTGTCGGAGCTGAGTGAAGAGTGAAGCGGCTGAATCTCGACCGACGCGAG 1588
Db 1321 GACCGCATATTGTCGGAGCTGAGTGAAGAGTGAAGCGGCTGAATCTCGACCGACGCGAG 1380
Qy 1589 CTGTCTCTGCTCAAGGCCATCATCTGTACAAACCGGACATACGCGGGATCAAGAGCCGG 1648
Db 1381 CTGTCTCTGCTCAAGGCCATCATCTGTACAAACCGGACATACGCGGGATCAAGAGCCGG 1440
Qy 1649 GCGGAGATCGAGATGTGCGCGGAGAGGTGTACGCTTGCTTGGAGAGCAGCTGCGCGCTG 1708
Db 1441 GCGGAGATCGAGATGTGCGCGGAGAGGTGTACGCTTGCTTGGAGAGCAGCTGCGCGCTG 1500
Qy 1709 GAAATATCCGGGCGACGATGCGCGGAGAGGTGTACGCTTGCTTGGAGAGCAGCTGCGCGCTG 1767
Db 1501 GAAATATCCGGGCGACGATGCGCGGAGAGGTGTACGCTTGCTTGGAGAGCAGCTGCGCGCTG 1560
Qy 1768 ATCGATCAGCCTGAAAGTGCAGGATCACTGTTCCTCTTCCGCAATTACCGAGCGCGGC 1827
Db 1561 ATCGATCAGCCTGAAAGTGCAGGATCACTGTTCCTCTTCCGCAATTACCGAGCGCGGC 1620
Qy 1828 GCTGAGGAGAGCTCTTTCTCGAGCAGCTGGAGCGCGCGCCACCGCGCTGCGCATGAA 1887
Db 1621 GCTGAGGAGAGCTCTTTCTCGAGCAGCTGGAGCGCGCGCCACCGCGCTGCGCATGAA 1680
Qy 1888 ACTGAGTAGGGTCCCGACTCTAAAGTCTGCCCGTTCTCCATCCGAAATGTTTCATT 1947
Db 1681 ACTGAGTAGGGTCCCGACTCTAAAGTCCGCCCGCTTCTCCATCCGAAATGTTTCATT 1740
Qy 1948 GTGATGCGTTGTTGTGCACTTCTCTCTATCCCTTATACCTTACAAAGCCCGCTTAA 2007
Db 1741 GTGATGCGTTGTTGTGCACTTCTCTCTAT-----CCCTACAAAGCCCGCTTAA 1792
Qy 2008 TATTACGCAAAATGTATGTAAATGTTTATTTTTTTTTTTTATTTACTAATATTTATTTA 2067
Db 1793 TATTACGCAAAATGTATGTAAATGTTTATTTTTTTTTTTTATTTACTAATATTTATTTA 1852
Qy 2068 TTATTGATATAGAAATGTTTCTTAAAGTGAAGATTAGCTCTCGACGTTTATGTC 2127
Db 1853 TTATTGATATAGAAATGTTTCTTAAAGTGAAGATTAGCTCTCGACGTTTATGTC 1912
Qy 2128 CAGTAAACGAAACAAACAAATCCAAACTTTGAAAGAGACACAAACACGAAACGAGAA 2187
Db 1913 CAGTAAACGAAACAAACAAATCCAAACTTTGAAAGAGACACAAACACGAAACGAGAA 1972
Qy 2188 AATGCACAAAGCAAAAGTAAAGTAAAGTAAAGCTAAAGCTAAAGCTAAAGATATTA 2247
Db 1973 AATGCACAAAGCAAAAGTAAAGTAAAGTAAAGCTAAAGCTAAAGCTAAAGATATTA 2032
Qy 2248 AAATAACGGTTAAATTAATGCATAGTTATGATCTACAGAGTATGTAAACATACAAAT 2307
Db 2033 AAATAACGGTTAAATTAATGCATAGTTATGATCTACAGAGTATGTAAACATACAAAT 2092
Qy 2308 CAGCATAAATATATATGTACGAGCGCATATCTGCGGTGTGCGCCCGTCTTAATCNA 2367
Db 2093 CAGCATAAATATATATGTACGAGCGCATATCTGCGGTGTGCGCCCGTCTTAATCNA 2152
Qy 2368 TTGTAAATTTACTTTTTTAACATAAAATTTACCCAAAAGTTTATCAATTAGATGCGAGATACA 2427
Db 2153 TTGTAAATTTACTTTTTTAACATAAAATTTACCCAAAAGTTTATCAATTAGATGCGAGATACA 2212
Qy 2428 AAATCACCGACGAAACCAACAAATATATCTATGTATAAAAATATATAACTGCATAACA 2487
Db 2213 AAATCACCGACGAAACCAACAAATATATCTATGTATAAAAAATATATAAGCTGCATAACA 2272
Qy 2488 A 2488
Db 2273 A 2273

QY 1409 GGCACGATGGCTCTCTTTCAGCGACGATCACCGGGCCTTTCAGCCCGCAGCTGTTCTTC 1468
Db |||||
QY 1469 AACCCAGAGCTCTCGTACCATCGACAGTGGATCAAGCCGGTGTGTGACGCATCTTC 1528
Db |||||
QY 1529 GACCGCATATCTCGGAGCTGAGTGTAAAGATGAAGCGCTGAATCTCGACCGACGCGAG 1588
Db |||||
QY 1589 CTGTCTCTGTTGAAGCCCATCATCTGTATAACCCCGGACATACGCGGGATCAAGACCGG 1648
Db |||||
QY 1649 GCGGAGATCGAGATGCGCGGAGAGGTGACGCTTGCTGCTGAGCAGACACTGCGCCTG 1708
Db |||||
QY 1709 GAAACATCCGGGCGACGATGAGACGCTTTGGCGCACTGCTGCTGCTGC- CGCTTTTGG 1767
Db |||||
QY 1768 ATCGATCAGCTGAAAGTCCAGGATCACCTGTTCTCTTCCGCTATTACGAGCGACCGCC 1827
Db |||||
QY 1828 GCTGAGGAGCTCTTCTCGAGCAGCTGAGCGCGCGCGCCACCGCGCTGGCGATGAA 1887
Db |||||
QY 1888 ACTGAGTAGGCTCCGAGCTCTAAAGTCTCCCGCTTCTCCATCCGAAAAATGTTTCATT 1947
Db |||||
QY 1948 GTGATTGCTGTTTGTGCAATTTCTCTCTCTATCCCTTATACCTTACAAAAGCCCTTAA 2007
Db |||||
QY 2008 TATTACGCAAAATGTATGTAATTTGTTATTTTATTTTATTTTATTTTATTTATTTATTTA 2067
Db |||||
QY 2068 TTATTGATATAGAAATGTTTTCCTTAAGATGAAGTTCCTCGACGTTTATGTCC 2127
Db |||||
QY 2128 CAGTAAACGAAAAACAAACAAATCCAAACCTTGAAGAGAACACAAAAACAGCAGAA 2187
Db |||||
QY 2188 AATGACACAGCAAAAGTAAAGTTAAAGTTAAAGTTAAAGTTAAAGTTAAAGTTAAAGTTA 2247
Db |||||
QY 2248 AAATAACGGTTAAATTAATGATAGTTATGATCTACAGAGCTATGTAACATACAAATTT 2307
Db |||||
QY 2308 CAGCATAAATATATATGTGACGAGCGCATATCTCGGTGCTGCGCCCGTTCTTAATCAA 2367
Db |||||
QY 2368 TTGTAATTTACTTTTAAACATAAAATTTACCCAAACGTTTATCAATTTAGATGCGAGATCAA 2427
Db |||||
QY 2428 AAATCACCAGCAAAACCAACAAATATATCTATGTATATAAAATATATAAATCTGCATAACA 2487
Db |||||
QY 2487 AAATCACCAGCAAAACCAACAAATATATCTATGTATATAAAATATATAAATCTGCATAACA 2547
Db |||||

QY 2488 A 2488
Db 2273 A 2273

RESULT 10
AAT89959
ID AAT89959 standard; DNA; 2304 BP.
XX
AC AAT89959;
XX
DT 19-MAR-1998 (first entry)
XX
DE D. melanogaster XR2C retinoid-like receptor DNA.
XX
KW Retinoid-like receptor; XR2C; insecticide; RXR-alpha; transcription;
ultraspiracle locus; steroid/thyroid receptor superfamily; ss.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
CDS 163..1704
FT /*tag= a
FT /product= "XR2C"
FT /note= "retinoid-like receptor"
XX
PN US5688691-A.
XX
PD 18-NOV-1997.
XX
PF 05-JUN-1995; 95US-00464272.
XX
PR 22-MAR-1990; 90US-00497935.
XX
PR 04-FEB-1993; 93US-00013975.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Oro AE, Evans RM;
XX
DR WPI; 1998-007984/01.
XX
DR P-PSDB; AAW31320.
XX
PT DNA encoding insect retinoid-like receptor - used to transform insect
cells for insecticide screening.
XX
PS Claim 1; Col 9-14; 11pp; English.
XX
CC This DNA sequence encodes an novel retinoid-like receptor protein XR2C
which is structurally and functionally related to the steroid/thyroid
superfamily of receptors. This gene is substantially similar to mammalian
RXR-alpha receptors which are activated to modulate transcription of
certain genes in cells when the cells are exposed to retinoic acid and
has been mapped to the Drosophila ultraspiracle locus. This receptor can
be used to screen for compounds of potential value as insecticides
XX
SQ Sequence 2304 BP; 631 A; 619 C; 603 G; 451 T; 0 U; 0 Other;

Query Match 90.0%; Score 2238.2; DB 2; Length 2304;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 3; Indels 9; Gaps 2;

QY 209 GGACACGCTGCGCTTGGCAAGTGAACCCCAACAGAGAGCGAAAGCGAGCGAGCGCTGCC 268
Db 1 GGACACGCTGCGCTTGGCAAGTGAACCCCAACAGAGAGCGAAAGCGAGCGAGCGACAC 60
QY 269 ACCACATACACAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 328
Db 61 ACCACATACACAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 120
QY 329 CCAGTTCTTCAATATATACCCAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 388
Db 121 CCAGTTCTTCAATATATACCCAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 180

Qy	389	GACGCCAGCTTTTCGCTGAGCCACATCAAGGAGGAGGTCAAGCCGGACATCTCGAGCTG	448
Db	181	GACGCCAGCTTTTCGCTGAGCCACATCAAGGAGGAGGTCAAGCCGGACATCTCGAGCTG	240
Qy	449	AACGACAGCAACAACAGCAGCTTTTCGCTGAGCCAGGAGTCCCGTTCATGCAG	508
Db	241	AACGACAGCAACAACAGCAGCTTTTCGCTGAGCCAGGAGTCCCGTTCATGCAG	300
Qy	509	GCCATGTCATGCTTCAGCTGCTGCGCGCTCCAACTCCGCGAGCTCCAAACAAACAGC	568
Db	301	GCCATGTCATGCTTCAGCTGCTGCGCGCTCCAACTCCGCGAGCTCCAAACAAACAGC	360
Qy	569	GCTGAGATGCCAAATGCGCGAGCGCCCAATTCGCTGAGGCTCTGCGCGCTGCA	628
Db	361	GCTGAGATGCCAAATGCGCGAGCGCCCAATTCGCTGAGGCTCTGCGCGCTGCA	420
Qy	629	GTCCAGCAGCAGTATCCGCTTAACCATCCGCTGAGCGGACAGCAACCTCTGCTTATT	688
Db	421	GTCCAGCAGCAGTATCCGCTTAACCATCCGCTGAGCGGACAGCAACCTCTGCTTATT	480
Qy	689	TGCGGGATCCGCGCAGTGGCAAGCACTACCGCTGTACAGCTGTGAGGCTGCAAGGC	748
Db	481	TGCGGGATCCGCGCAGTGGCAAGCACTACCGCTGTACAGCTGTGAGGCTGCAAGGC	540
Qy	749	TTCTTTAAACGACACAGTCCGCAAGGATCTCACATACGCTTCGAGGAGAACCGCACTGC	808
Db	541	TTCTTTAAACGACACAGTCCGCAAGGATCTCACATACGCTTCGAGGAGAACCGCACTGC	600
Qy	809	ATCATAGACAAAGCGCAGAGGAAACGCTTCAGTATCGCCGCTACCAAGATGCTTAACC	868
Db	601	ATCATAGACAAAGCGCAGAGGAAACGCTTCAGTATCGCCGCTACCAAGATGCTTAACC	660
Qy	869	TGCGGATGAGCGGAGACCGCTCCAGGAGAGCGTCAACCGGCGCCGCAATGCGGCG	928
Db	661	TGCGGATGAGCGGAGACCGCTCCAGGAGAGCGTCAACCGGCGCCGCAATGCGGCG	720
Qy	929	GGTAGGCTCAGCGCAGCGAGGCGGAGTAGCGTCCAGGTTGCGTAGGCGGATCCAGC	988
Db	721	GGTAGGCTCAGCGCAGCGAGGCGGAGTAGCGTCCAGGTTGCGTAGGCGGATCCAGC	780
Qy	989	TCTCAAGCGGAGGAGGAGGCGGCTTTCTGCGGAATGGGACGCGCAACGGTTCT	1048
Db	781	TCTCAAGCGGAGGAGGAGGCGGCTTTCTGCGGAATGGGACGCGCAACGGTTCT	840
Qy	1049	GATGATCTTCATGACCAATAGCGTGTCCAGGATTTCTCGATCGAGCGCATATAGAGCC	1108
Db	841	GATGATCTTCATGACCAATAGCGTGTCCAGGATTTCTCGATCGAGCGCATATAGAGCC	900
Qy	1109	GAGCAGCAGCGGAGACCAATGCGCGATCGTGCACTGACGTTCTCGCGGTTGGTCCC	1168
Db	901	GAGCAGCAGCGGAGACCAATGCGCGATCGTGCACTGACGTTCTCGCGGTTGGTCCC	960
Qy	1169	TATTCACAGTCCAGCGGACTACAAAGGCTGCGTGTGCGCCCTGTGCAAGTGGTCAAC	1228
Db	961	TATTCACAGTCCAGCGGACTACAAAGGCTGCGTGTGCGCCCTGTGCAAGTGGTCAAC	1020
Qy	1229	AAACAGCTCTTCCAGATGGTGAATACCGCGCATGATGCGGCATTTGCGCGAGTGGCG	1288
Db	1021	AAACAGCTCTTCCAGATGGTGAATACCGCGCATGATGCGGCATTTGCGCGAGTGGCG	1080
Qy	1289	CTGGACGACGAGTGAATCTGCTGAAAGCGCTTGGATCGAGCTGCTCATTTGCCAAGCTG	1348
Db	1081	CTGGACGACGAGTGAATCTGCTGAAAGCGCTTGGATCGAGCTGCTCATTTGCCAAGCTG	1140
Qy	1349	GCCTGGTGCAGCATCGTTTCGCTGGATGACGCGGCTGCGCGCGCGCGGCGGTGACTA	1408
Db	1141	GCCTGGTGCAGCATCGTTTCGCTGGATGACGCGGCTGCGCGCGCGCGGCGGTGACTA	1200
Qy	1409	GGCCAGATGGTCTTTGAGGAGCAGATCACCGGCGCTTCAGCCCGCAGCTGTCTCTC	1468
Db	1201	GGCCAGATGGTCTTTGAGGAGCAGATCACCGGCGCTTCAGCCCGCAGCTGTCTCTC	1260
Qy	1469	AACCAGAGCTTCTCGTACCATCGCAACAGTGCATCAAAAGCGGCTGTGTGAGCCATCTTC	1528

RESULT 11

Db	1261	AACCAGAGCTTCTCGTACCATCGCAACAGTGCATCAAAAGCCGCTGTGTGAGCCATCTTC	1320
Qy	1529	GACCGCATATTTGTCGGAGCTGAGTTAAAGATGAAGCGGCTGAATCTCGACCGACGCGAG	1588
Db	1321	GACCGCATATTTGTCGGAGCTGAGTTAAAGATGAAGCGGCTGAATCTCGACCGACGCGAG	1380
Qy	1589	CTGTCCTGCTTGAAGGCGCATACTACTGTACAAACCGGACATACGCGGATCAAGAGCCGG	1648
Db	1381	CTGTCCTGCTTGAAGGCGCATACTACTGTACAAACCGGACATACGCGGATCAAGAGCCGG	1440
Qy	1649	GCGGAGATCGAGATGTGCGCGGAGAGGTGACGCTTTCGCTGGAAGCACTGCGCGCTG	1708
Db	1441	GCGGAGATCGAGATGTGCGCGGAGAGGTGACGCTTTCGCTGGAAGCACTGCGCGCTG	1500
Qy	1709	GAACATCCGGGCGAGTGAACGCTTTGCGCAACTGCTGCTGCGTCTGCGCGCTTTGCG	1767
Db	1501	GAACATCCGGGCGAGTGAACGCTTTGCGCAACTGCTGCTGCGTCTGCGCGCTTTGCG	1560
Qy	1768	ATCGATCAGCTCTGAAGTGCAGGATCACCTGTTCTCTTCGCGATTAACGAGCGACCGGCC	1827
Db	1561	ATCGATCAGCTCTGAAGTGCAGGATCACCTGTTCTCTTCGCGATTAACGAGCGACCGGCC	1620
Qy	1828	GCTGGAGGAGCTCTTTCTCGAGCAGCTGGAGGCGCGCCGCCACCCGCGCTTGCGCATGAA	1887
Db	1621	GCTGGAGGAGCTCTTTCTCGAGCAGCTGGAGGCGCGCGGCCACCCGCGCTTGCGCATGAA	1680
Qy	1888	ACTGGAGTAGGCTCCCGACCTAAAGTCTCCCGGTTCTCCATCCGAAAAATGTTTCATT	1947
Db	1681	ACTGGAGTAGGCTCCCGACCTAAAGTCTCCCGGTTCTCCATCCGAAAAATGTTTCATT	1740
Qy	1948	GTGATTCGCTTGTGTCATTTCTCCTCTCTATCCCTTATACCCCTACAAAAGCCCCCTAA	2007
Db	1741	GTGATTCGCTTGTGTCATTTCTCCTCTCTAT-----CCCTACAAAAGCCCCCTAA	1792
Qy	2008	TATTAACGCAAAATGTGTATTAATTTTATTTTATTTTATTTTATTTTATTTATTTATTA	2067
Db	1793	TATTAACGCAAAATGTGTATTAATTTTATTTTATTTTATTTTATTTATTTATTTATTA	1852
Qy	2068	TTATTGATATAGAAAATGTTTTCTTAAGATGAAGATTAGCCTCTCGAGTTTATGTC	2127
Db	1853	TTATTGATATAGAAAATGTTTTCTTAAGATGAAGATTAGCCTCTCGAGTTTATGTC	1912
Qy	2128	CAGTAAACGAAAAACAAAATCCAAAATCTTGAAAAAGAACACAAAACACGAAACGAGAA	2187
Db	1913	CAGTAAACGAAAAACAAAATCCAAAATCTTGAAAAAGAACACAAAACACGAAACGAGAA	1972
Qy	2188	AATGCACACAAAGCAAAAGTAAAGTTAAACTAAAGCTAAACGAGTAAAGATATTA	2247
Db	1973	AATGCACACAAAGCAAAAGTAAAGTTAAACTAAAGCTAAACGAGTAAAGATATTA	2032
Qy	2248	AAATAACGGTTAAATAATTAATGTCATAGTATGATCTACAGAGTATGTAACATACAAAT	2307
Db	2032	AAATAACGGTTAAATAATTAATGTCATAGTATGATCTACAGAGTATGTAACATACAAAT	2092
Qy	2308	CAGCATAAATATATATCTGACGAGCGCATATCTGCGGTGCTGCGCCCGTTCTAAATCAA	2367
Db	2093	CAGCATAAATATATATGTCAGGCGCGCATATCTGCGGTGCTGCGCCCGTTCTAAACCAA	2152
Qy	2368	TTGTAATTTACTTTTTTAAATAAATTTTAAACCAAAACGTTATCAATTAGATGCGAGATCAA	2427
Db	2153	TTGTAATTTACTTTTTTAAACATAAATTTTAAACCAAAACGTTATCAATTAGATGCGAGATCAA	2212
Qy	2428	AAATCAGCGAGAAAAACCAAAATATATCTATGATATAAAATATATAAATGTCATACAA	2487
Db	2213	AAATCAGCGAGAAAAACCAAAATATATCTATGATATAAAATATATAAATGTCATACAA	2272
Qy	2488	A 2488	
Db	2273	A 2273	

Qy	1310	CTGAAAGCCGCTTGGATCGAGCTGCTCATTTGCCGAACGTGGCTGGTGCAGCATCGTTTCG	1369
Db	241	CTGAAAGCCGCTTGGATCGAGCTGCTCATTTGCCGAACGTGGCTGGTGCAGCATCGTTTCG	300
Qy	1370	CTGGATGACGGCGGTGTCGGGGGGGGGGGGGGTGGAGCTAGGCCACGATGGCTCCTTTTGAG	1429
Db	301	CTGGATGACGGCGGTGTCGGGGGGGGGGGGGGTGGAGCTAGGCCACGATGGCTCCTTTTGAG	360
Qy	1430	CGACGATCACCGGCGCTTCAGCGCCACGACGCTGTTCCTCAACACGAGAGCTTCTCGTACCAT	1489
Db	361	CGACGATCACCGGCGCTTCAGCGCCACGACGCTGTTCCTCAACACGAGAGCTTCTCGTACCAT	420
Qy	1490	CGCAACAGTGCATCAAAAGCCGGTGTCTGAGCCATCTTCGACCGCATATTGTTCGGAGCTG	1549
Db	421	CGCAACAGTGCATCAAAAGCCGGTGTCTGAGCCATCTTCGACCGCATATTGTTCGGAGCTG	480
Qy	1550	AGTGTAAGATGAAGCGCGCTGAATCTCGACCGACGAGCTGTCTCTCTTGAAGGCCATC	1609
Db	481	AGTGTAAGATGAAGCGCGCTGAATCTCGACCGACGAGCTGTCTCTCTTGAAGGCCATC	540
Qy	1610	ATACTGTACAAACCGGCATACCGGGATCAAGAGCCGGCGGAGATCGAGATGTGCCG	1669
Db	541	ATACTGTACAAACCGGCATACCGGGATCAAGAGCCGGCGGAGATCGAGATGTGCCG	600
Qy	1670	GAGAAGGTGTACGCTTGCCTTGACGAGCACTGCCGCTTGGAAACATCCGGGCGAGATGGA	1729
Db	601	GAGAAGGTGTACGCTTGCCTTGACGAGCACTGCCGCTTGGAAACATCCGGGCGAGATGGA	660
Qy	1730	CGCTTTGCGCAACTGCTGTGCGTCTGCCCGCTTTGGCGATCGATCAGCCTGAAGTGCAG	1789
Db	661	CGCTTTGCGCAACTGCTGTGCGTCTGCCCGCTTTGGCGATCGATCAGCCTGAAGTGCAG	720
Qy	1790	GATCACCTGTTCTCTTCGCCATTACAGAGCCGGCGGATCGAGATGTGCCG	1849
Db	721	GATCACCTGTTCTCTTCGCCATTACAGAGCCGGCGGATCGAGATGTGCCG	780
Qy	1850	CAGCTGGAGCGCGCGCCACCGGCTTGGCGATGAAATCGGAG	1894
Db	781	CAGCTGGAGCGCGCGCCACCGGCTTGGCGATGAAATCGGAG	825
RESULT 12			
ABT08312			
ID			
ABT08312 standard; DNA; 825 BP.			
AC			
ABT08312;			
XX			
28-NOV-2002 (first entry)			
XX			
ECR-based inducible gene expression cassette related DNA SEQ ID No 60.			
DE			
Gene expression modulation system; large-scale production; gene therapy;			
KW			
gene expression cassette; functional genomics; transgenic organism; ds.			
KW			
XX			
Drosophila melanogaster.			
OS			
XX			
WO200266613-A2.			
PN			
XX			
29-AUG-2002.			
PD			
XX			
20-FEB-2002; 2002WO-US005235.			
PF			
XX			
20-FEB-2001; 2001US-0269799P.			
PR			
31-MAY-2001; 2001US-0294814P.			
PR			
(ROHM) ROHM & HAAS CO.			
XX			
PA			
XX			
Palli SR, Kapitskaya MZ;			
PI			
XX			
WFI; 2002-674929/72.			
DR			
XX			
Novel ecdysone receptor/invertebrate retinoid X receptor-based inducible			
PT			

PT gene expression system useful for modulating gene expression in host cell
XX for gene therapy and large-scale production of proteins and antibodies.
PS Example 1; Page 123; 123pp; English.

XX The invention relates to a novel gene expression modulation system
XX comprising first and second gene expression cassettes that comprises
XX polynucleotides encoding first and second hybrid polypeptides. The gene
XX expression modulation system is useful for modulating the expression of a
XX gene in a host cell comprising the gene to be modulated, for applications
XX such as gene therapy, large-scale production of proteins and antibodies,
XX cell-based high throughput screening assays, functional genomics and
XX regulation of traits in transgenic organisms. This polynucleotide
XX sequence represents DNA relating to the gene expression cassettes of the
XX invention

SQ Sequence 825 BP; 158 A; 248 C; 258 G; 161 T; 0 U; 0 Other;
Query Match 33.2%; Score 825; DB 6; Length 825;
Best Local Similarity 100.0%; Pred. No. 1.4e-173; Indels 0; Gaps 0;
Matches 825; Conservative 0; Mismatches 0;

QY 1070 GTGTCCAGGGATTTCGATCGAGCGCATATAGAGCCGAGCGAGCGAGACCCAA 1129
DB 1 GTGTCCAGGGATTTCGATCGAGCGCATATAGAGCCGAGCGAGCGAGACCCAA 60
QY 1130 TGGCGGATCTGCACTGACGTTCTGCGCGTTGGTCCCTATTCACAGTCCAGCCGAC 1189
DB 61 TGGCGGATCTGCACTGACGTTCTGCGCGTTGGTCCCTATTCACAGTCCAGCCGAC 120
QY 1190 TACAAGGCGTGTGTCGCGCCCTGTGCCAAGTGTCAACAAACAGCTCTCCAGATGGTC 1249
DB 121 TACAAGGCGTGTGTCGCGCCCTGTGCCAAGTGTCAACAAACAGCTCTCCAGATGGTC 180
QY 1250 GAATACGCGCGATGATCCGACATTTGCCAGGTGCGCTGGACGACAGGTGATCTG 1309
DB 181 GAATACGCGCGATGATCCGACATTTGCCAGGTGCGCTGGACGACAGGTGATCTG 240
QY 1310 CTGAAGCGGCTTGGATCGAGTCTCATTTGCGAACGTTGGCTGGTGCAGCATCGTTTCG 1369
DB 241 CTGAAGCGGCTTGGATCGAGTCTCATTTGCGAACGTTGGCTGGTGCAGCATCGTTTCG 300
QY 1370 CTGATGACGCGCGGTGCGCGCGCGGGCGGTGGACTAGGCCACGATGGCTCTTTGAG 1429
DB 301 CTGATGACGCGCGGTGCGCGCGCGGGCGGTGGACTAGGCCACGATGGCTCTTTGAG 360
QY 1430 CGAGCATCACCGGGCTTCAGCCCCAGCAGGTGTTCTCAACAGAGTTTCTGTACCAT 1489
DB 361 CGAGCATCACCGGGCTTCAGCCCCAGCAGGTGTTCTCAACAGAGTTTCTGTACCAT 420
QY 1490 CGCACAGTGCATCAAGCCGGTGTGTCAGCCATCTTCGACCGCATATTTGCGAGCTG 1549
DB 421 CGCACAGTGCATCAAGCCGGTGTGTCAGCCATCTTCGACCGCATATTTGCGAGCTG 480
QY 1550 AGTGTAAAGATGAAGCGCTGAATCTCGACCGAGCGAGTGTCTGCTGTAAGGCCCATC 1609
DB 481 AGTGTAAAGATGAAGCGCTGAATCTCGACCGAGCGAGTGTCTGCTGTAAGGCCCATC 540
QY 1610 ATACTGTACAACCCCGACATACGCGGGATCAAGAGCCGCGGAGATCGAGATGTGCGC 1669
DB 541 ATACTGTACAACCCCGACATACGCGGGATCAAGAGCCGCGGAGATCGAGATGTGCGC 600
QY 1670 GAGAAGGTGTAGCTTGTCTGACGAGCATCTGCGCCCTGGAAACATCCGGGCGACGATGGA 1729
DB 601 GAGAAGGTGTAGCTTGTCTGACGAGCATCTGCGCCCTGGAAACATCCGGGCGACGATGGA 660
QY 1730 CGCTTTGCGCAACTGCTGCTGCGTCTGCGCGCTTTGGATCGATCAGCTCTGAAGTGCAG 1789
DB 661 CGCTTTGCGCAACTGCTGCTGCGTCTGCGCGCTTTGGATCGATCAGCTCTGAAGTGCAG 720
QY 1790 GATCACCTGTTCTCTTCGCAATACAGCGACCGCGCGCTGGAGAGCTCTTTCTCGAG 1849
DB 721 GATCACCTGTTCTCTTCGCAATACAGCGACCGCGCGCTGGAGAGCTCTTTCTCGAG 780

QY 1850 CAGCTGAGGCGCGCGCCACCGCGCTGGCGATGAAACTGGAG 1894
DB 781 CAGCTGAGGCGCGCGCCACCGCGCTGGCGATGAAACTGGAG 825

RESULT 13
ACC00562
ID ACC00562 standard; DNA; 799 BP.

XX AC ACC00562;

XX 23-JUN-2003 (first entry)

XX Drosophila ultraspiracle protein (CfUSP) EF domain polynucleotide.

XX Ecdysone receptor; BaEcr; pesticide; insect; male sterility; whitefly;
XX ultraspiracle protein; USP; fruitfly; EF domain; ds.

XX Drosophila melanogaster.

XX W02003027266-A2.

XX 03-APR-2003.

XX 20-FEB-2002; 2002WO-US005234.

XX 26-SEP-2001; 2001US-0325534P.

XX (ROHM) ROHM & HAAS CO.

XX Zhang J, Cress DE, Palli SR, Dhadialla TS;

XX WPI; 2003-342734/32.

XX Novel isolated whitefly (Bemisia argentifoli) ecdysone receptor
XX polypeptide, useful for screening for molecules e.g., agonist or
XX antagonist of ecdysone receptor activity in a cell, which are useful as
XX pesticides.

XX Example 2; Page 80-81; 85pp; English.

XX The invention relates to a whitefly (Bemisia argentifoli) ecdysone
XX receptor (BaEcr) polypeptide and encoding polynucleotides. The BaEcr
XX polypeptide and polynucleotides are useful for modulating gene expression
XX in an ecdysone receptor-based gene expression system, and for identifying
XX and selecting ligands specific for binding to a ligand-binding domain of
XX BaEcr, and for identifying and selecting compounds exhibiting specific
XX binding to the ligand binding domain of BaEcr. Agonists and antagonists
XX of BaEcr modulate insect physiology and development, thus modifying the
XX normal temporal sequence of developmental agents in an insect. For
XX example, accelerating insect development can be achieved for instance in
XX producing sterile males. Alternatively, it may be useful slow development
XX in pest infestation, such that the insects reach destructive stages of
XX development only after commercial crops may have passed sensitive stages.
XX The agonists and antagonists are also useful for artificially maintaining
XX insects in a specific developmental stage. The present sequence
XX represents a Drosophila ultraspiracle protein (dmUSP) EF domain encoding
XX expression cassettes

XX Sequence 799 BP; 154 A; 241 C; 250 G; 154 T; 0 U; 0 Other;

Query Match 32.1%; Score 799; DB 8; Length 799;
Best Local Similarity 100.0%; Pred. No. 8.6e-168;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 CATAGAGCGCGAGCGAGCGAGACCCCAATGCGCGATCGTGCACTGACGTTCTCTGCG 1158
DB 1 CATAGAGCGCGAGCGAGCGAGACCCCAATGCGCGATCGTGCACTGACGTTCTCTGCG 60

QY 1159 CGTTGGTCCCTATTCCACAGTCCAGCGGACTCAAGGGTGCCTGTGCGCCCTGTGCCA 1218
DB 1159 CGTTGGTCCCTATTCCACAGTCCAGCGGACTCAAGGGTGCCTGTGCGCCCTGTGCCA 1218

Db 61 CGTGTGTCCTATTCCACAGTCAGCCGCGACTACAAGGGTGCCTGTGCGCCCTGTGCGCA 120
Qy 1219 AGTGTGTCACAAACAGCTCTTCCAGATGTCGAATACGCGCGCATGATCGCGCACTTTCG 1278
Db 121 AGTGTGTCACAAACAGCTCTTCCAGATGTCGAATACGCGCGCATGATCGCGCACTTTCG 180
Qy 1279 CAGGTGCGCTGGACGACAGGTGATTCGTGTAAGCGCTTGGATCGAGCTGCTCAT 1338
Db 181 CCAGGTGCGCTGGACGACAGGTGATTCGTGTAAGCGCTTGGATCGAGCTGCTCAT 240
Qy 1339 TCGAACGTGGCTGTGTCAGCATCGTTTTCGTGATGACGCGGTGCGCGCGGGGG 1398
Db 241 TCGAACGTGGCTGTGTCAGCATCGTTTTCGTGATGACGCGGTGCGCGCGGGGG 300
Qy 1399 CGGTGACTAGGCCAGATGGCTCTTTGAGCGACGATCACCGGGCTTTCAGCCCCAGCA 1458
Db 301 CGGTGACTAGGCCAGATGGCTCTTTGAGCGACGATCACCGGGCTTTCAGCCCCAGCA 360
Qy 1459 GCTGTTCTCAACGAGCTTCTGTACCATCGATCGCAACAGTGGCATCAAGCGGTGTGC 1518
Db 361 GCTGTTCTCAACGAGCTTCTGTACCATCGCAACAGTGGCATCAAGCGGTGTGC 420
Qy 1519 AGCCATCTTCGACCGCATATTGTCGAGCTGATGTAAAGATGAAGCGGTGAATCTCGA 1578
Db 421 AGCCATCTTCGACCGCATATTGTCGAGCTGATGTAAAGATGAAGCGGTGAATCTCGA 480
Qy 1579 CCGAGCGGAGCTGCTGCTGTAAGGCCATCATCTGTACAAACCGGACATACGCGGAT 1638
Db 481 CCGAGCGGAGCTGCTGCTGTAAGGCCATCATCTGTACAAACCGGACATACGCGGAT 540
Qy 1639 CAAAGCGCGGCGGAGATCGAGATGTGCGCGAGAGGTGTACGTTGCTCGACGAGCA 1698
Db 541 CAAAGCGCGGCGGAGATCGAGATGTGCGCGAGAGGTGTACGTTGCTCGACGAGCA 600
Qy 1699 CTGCGCGCTGGAACATCCGGCGAGTGGAGCTTTGCGCAACTGCTGCTGCTGCTGCC 1758
Db 601 CTGCGCGCTGGAACATCCGGCGAGTGGAGCTTTGCGCAACTGCTGCTGCTGCTGCC 660
Qy 1759 CGCTTTGCGCATCGATCAGCTGAAAGTGCCAGGATCACCTGTTCTCTTCCGCAATTACCA 1818
Db 661 CGCTTTGCGCATCGATCAGCTGAAAGTGCCAGGATCACCTGTTCTCTTCCGCAATTACCA 720
Qy 1819 CGACCGCGCTGGAGGAGCTCTTTCTCGAGAGCTGGAGGCGCGCGCCGCCACCGCGCT 1878
Db 721 CGACCGCGCTGGAGGAGCTCTTTCTCGAGAGCTGGAGGCGCGCGCGCCGCCACCGCGCT 780
Qy 1879 GCGGATGAAGTGGAGTAG 1897
Db 781 GCGGATGAAGTGGAGTAG 799

RESULT 14
ACC71950
ID ACC71950 standard; DNA; 799 BP.
XX
AC ACC71950;
XX
DT 04-AUG-2003 (first entry)
XX
DE D. melanogaster ultraspiracle protein (DMUSP) EF domain DNA.
XX
KW EcR; NcEcR; leafhopper; ecdysone receptor; homopteran; insecticide;
XX gene expression; ultraspiracle protein; USP; EF domain; ds.
XX
OS Drosophila melanogaster.
XX
FN WO2003027289-A1.
XX
PD 03-APR-2003.
XX
PF 20-FEB-2002; 2002WO-US005026.
XX
PR 26-SEP-2001; 2001US-0325096P.

XX (ROHM) ROHM & HAAS CO.
XX Palli SR;
XX WPI; 2003-481913/45.
XX
XX Novel isolated leafhopper ecdysone receptor polypeptide from homopteran
XX green leafhopper e.g. Nephrotetix cincticeps, for identifying molecules
XX that modulate receptor activity and in insecticide discovery.
XX
XX Example 2; Page 76; 81pp; English.
XX
XX The invention relates to an isolated leafhopper ecdysone receptor
XX polypeptide (NcEcR) from the homopteran green leafhopper (Nephrotetix
XX cincticeps) and encoding polynucleotide. The NcEcR polypeptide, and
XX polynucleotide and vectors comprising the polynucleotide are useful in
XX the field of gene expression and insecticide discovery. The NcEcR
XX polypeptide and polynucleotide are useful for regulating gene expression
XX of a polypeptide of interest in a host cell and in identifying new
XX molecules that modulate activity of a leafhopper ecdysone receptor (EcR).
XX Specific antibodies are useful as a reagent for determining qualitative
XX or quantitative presence of the receptor and to separate or purify the
XX receptor. A composition comprising NcEcR polypeptide, polynucleotide and
XX vectors are useful for formulation of biological material for use in a
XX gene expression modulation system or a ligand-screening assay. Sequences
XX ACC71949-51 represent polynucleotides encoding the EF domains of the
XX ultraspiracle protein (USP) from various species
XX
XX Sequence 799 BP; 154 A; 241 C; 250 G; 154 T; 0 U; 0 Other;
XX
XX Query Match 32.1%; Score 799; DB 9; Length 799;
XX Best Local Similarity 100.0%; Pred. No. 8.6e-168;
XX Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1099 CATAGAGCCGAGCAGCGAGCGAGACCCAAATGGCGCATCGTCACTGACGTTCCTGCG 1158
Db 1 CATAGAGCCGAGCAGCGAGCGAGACCCAAATGGCGCATCGTCACTGACGTTCCTGCG 60
Qy 1159 CGTTGGTCCCTATTCCACAGTCCAGCGGACTACAGGGTGCCTGTGCGCCCTGTGCGCA 1218
Db 61 CGTTGGTCCCTATTCCACAGTCCAGCGGACTACAGGGTGCCTGTGCGCCCTGTGCGCA 120
Qy 1219 AGTGTGTCACAAACAGCTCTTCCAGATGTCGAATACGCGCGCATGATCGCGCACTTTCG 1278
Db 121 AGTGTGTCACAAACAGCTCTTCCAGATGTCGAATACGCGCGCATGATCGCGCACTTTCG 180
Qy 1279 CCAGGTGCGCTGGACGACCGAGGTGATTCGTGTAAGCGCTTGGATCGAGCTGCTCAT 1338
Db 181 CCAGGTGCGCTGGACGACCGAGGTGATTCGTGTAAGCGCTTGGATCGAGCTGCTCAT 240
Qy 1339 TCGAACGTGCGCTGGTGCAGCATCGTTTTCGTGATGACGCGGTGCGCGCGGGGG 1398
Db 241 TCGAACGTGCGCTGGTGCAGCATCGTTTTCGTGATGACGCGGTGCGCGCGGGGG 300
Qy 1399 CGGTGACTAGGCCAGCATGATGCTCTTTGAGCGACGATCACCGGGCTTTCAGCCCCAGCA 1458
Db 301 CGGTGACTAGGCCAGCATGATGCTCTTTGAGCGACGATCACCGGGCTTTCAGCCCCAGCA 360
Qy 1459 GCTGTTCTCAACGAGCTTCTGTACCATCGCAACAGTGGCATCAAGCGGTGTGC 1518
Db 361 GCTGTTCTCAACGAGCTTCTGTACCATCGCAACAGTGGCATCAAGCGGTGTGC 420
Qy 1519 AGCCATCTTCGACCGCATATTGTCGAGCTGATGTAAAGATGAAGCGGTGAATCTCGA 1578
Db 421 AGCCATCTTCGACCGCATATTGTCGAGCTGATGTAAAGATGAAGCGGTGAATCTCGA 480
Qy 1579 CCGAGCGGAGCTGCTGCTGTAAGGCCATCATCTGTACAAACCGGACATACGCGGAT 1638
Db 481 CCGAGCGGAGCTGCTGCTGTAAGGCCATCATCTGTACAAACCGGACATACGCGGAT 540
Qy 1639 CAAAGCGCGGCGGAGATCGAGATGTGCGCGAGAGGTGTACGTTGCTCGACGAGCA 1698
XX

Db 541 CAAGAGCGGCGGAGATCGAGATGTGCGCGAGAGGTGTACGTTGCGCTGGAGGAGCA 600
Qy 1699 CTGCGGCTGGAACATCCGGCGGAGTGGAGCGCTTTTCGCAACTGCTGCTGCTGCG 1758
Db 601 CTGCGGCTGGAACATCCGGCGGAGTGGAGCGCTTTTCGCAACTGCTGCTGCTGCG 660
Qy 1759 GCGTTTGGATCGATCAGCCTGAAAGTGCCAGGATCACCTGTTCTCTTCCGCATTACAG 1818
Db 661 GCGTTTGGATCGATCAGCCTGAAAGTGCCAGGATCACCTGTTCTCTTCCGCATTACAG 720
Qy 1819 CGACCGGCGCTGAGAGAGCTTTTCGAGCAGCTGGAGCGCGCGCCACCCGCGCT 1878
Db 721 CGACCGGCGCTGAGAGAGCTTTTCGAGCAGCTGGAGCGCGCGCCACCCGCGCT 780
Qy 1879 GCGGATGAACTGGAGTAG 1897
Db 781 GCGGATGAACTGGAGTAG 799
RESULT 15
AAF32133
ID AAF32133 standard; cDNA; 1536 BP.
XX AC AAF32133;
XX
XX 10-APR-2001 (first entry)
DT L cuprina USP subunit coding sequence SEQ ID NO: 7.
XX
DE Insect; steroid hormone receptor; juvenile hormone receptor; fly;
XX Ecr subunit; USP subunit; insecticide; ss.
XX
XX Lucilia cuprina.
XX
XX WO200102436-A1.
XX
XX 11-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-AU000799.
XX
XX 01-JUL-1999; 99US-00346470.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Hill RJ, Hannan GN;
XX
XX WPI; 2001-080981/09.
DR P-PSDB; AAB67099.
XX
XX New nucleic acid molecule for the regulation of gene expression in
PT insects.
XX
XX Claim 22; Page 130-132; 172pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC Bemisia tabaci (Silverleaf whitefly), Myzus persicae (aphid) and Lucilia
CC cuprina (sheep blowfly) steroid and juvenile hormone steroid receptor
CC subunits Ecr and USP. These can be used to screen for agents with
CC insecticidal activity
XX
SQ Sequence 1536 BP; 442 A; 326 C; 361 G; 407 T; 0 U; 0 Other;
Query Match 19.6%; Score 488.6; DB 4; Length 1536;
Best Local Similarity 64.3%; Pred. No. 1.9e-98;
Matches 796; Conservative 0; Mismatches 384; Indels 57; Gaps 2;
Qy 627 CAGTCCAGCAGCAGTATCGCTTACCACTACCTGAGCGGAGCAAGCACCTCTGCTCTA 686
Db 347 CACAACAGCAGCAGTATCCACCAATACCCCTTAGTGGTTCGNAACACTTGTGTTCA 406
Qy 687 TTTGCGGGATGGGCGCAGTGCAGCACTACGGCGTGTACAGTGTGAGGGGTGCAAGG 746
Db 407 TTTGTGGAGACCGCGCCAGTGGAAACATTATGGGGTCTACAGTTGTGAGGGTGTAAAG 466

Qy 747 GCTTCTTTAAACGACAGTGCAGGATCTCACATACGCTTGCGAGGAGAAACGCAACT 806
Db 467 GGTTCCTCAAACGATACGTTACGAGGACTTGTACATATGCTTGTGTGAGGACAGAATT 526
Qy 807 GCATCATAGACAAGCGCGCAGAGAAACCGCTGCGAGTACTGCCCGCTACCAAGTGCCTAA 866
Db 527 GCATTTATAGATAAACGACAAAGAAATCGTTGCCAGTATTGCTGTTATCAAAAGTGTTAG 586
Qy 867 CTGCGGCGATGAAGCGCGGAGCGGCTCCAGGAGGCGTCAACGGGCGCGCGCAATCGG 926
Db 587 CTTGTGCGCATGAACCGGAGCGGCTCCAGAGGAAACGACACGCTGCTGCTGCTA 646
Qy 927 CGGTAGGCTCAGCGCGAGCGGCGGAGTAGCGGTCCAGGTTCCGTTAGGCGGATCCA 986
Db 647 ACGCTA-----GAGCTG 658
Qy 987 GCTCTCAAGCGGAGGAGGAGGCGGCGCTTTCTGGCGAAATGGGAGCGGCAACGGTT 1046
Db 659 CTGCTGCTGCGGCTGGTGGAGGAGGTGGTGGGTAAAGCAATGTGTTGGTCTGGCG 718
Qy 1047 CTGATGACTTCATGACCAATAGCGTGTCCAGGAGTTTCTCGATCGAGCGCATCATAGG 1106
Db 719 GAGAAGACTTTAAACCCAGCAGTTCACTACGTGATCTCACTATAGAACCGCATCAATTGAAG 778
Qy 1107 CCGAGCAGCGAGCGGAGACCAATGCGGCGATCGTGCACTGACGTTCTTCTGCGGCTTGGTC 1166
Db 779 CCGAGCAAAAGGCTGAATCTTTGAGCGGTGTATACGTTGTGCTTTCGCGGCTGGCA 838
Qy 1167 CTTATTCACAGTCCAGCGGACTTACAAAGGTGCGGTGTCGCGCCCTGTGCAAGTGTGCA 1226
Db 839 ACAATTCATGTTAGCAACGACTTACAAAGCGCGGTATCTCATCTCTGCGAGATGGTTA 898
Qy 1227 ACAAACAGCTCTTCAGATGCTGGAATACGCGGCGCATGATGCGGCATTTTCCCGAGGTGC 1286
Db 899 ACAAACAACTCTACCAATGTTGAATATGACGCTCGAAACACCAATTTTACACATTTGC 958
Qy 1287 CGCTGGACGACGAGTGTATCTGCTGAAACGCTTGGATCGAGCTCTCATTCATTCGGAACG 1346
Db 959 AGCTGAGGATCAGATACATACTATTGTTAAAGCTGGCTGGATGAATGCTATTAATGCAATG 1018
Qy 1347 TGGCTGCTGTCAGCATCGTTTTCGCTGGATACGCGCGGTGCGCGGCGGCGGCGGTGAC 1406
Db 1019 TTGCTGCTGTCAGTATTGAGTCTCTGGATGCGGAATATGCT-----TCTCTGCTA 1069
Qy 1407 TAGCCACGATGCTCCTTTGAGCGGAGCATCACCGGCGCTTACGCGGAGCGAGCTGTTCC 1466
Db 1070 CGGTACATGACGCTTCTTTTGGTGGCGGTTTACCGAGTGCAGCGCCCAACACTCTTCC 1129
Qy 1467 TCACACGAGCTTCTCGTACCATCGCAACAGTGCATCAAAAGCGGTGTGTGACGCCATCT 1526
Db 1130 TTAATCAGAAATTTCTCGTATCATCGCAATAGTGTATTAAGGCCAATGTTGTTTCAATTT 1189
Qy 1527 TCGACCGCATATTTGTCGGAGCTGAGTGTAAAGATGAAGCGGCTGAATCTCGACCGAGCG 1586
Db 1190 TCGATGCTATCCTCTCGGAGTTGAGCATCAAAATGAAACGCTTTAAACATCGATCGCTCG 1249
Qy 1587 AGCTGCTGTTGAAGCGCATCATCTGTACAAACCGGAGCATACGCGGATCAAGAGCC 1646
Db 1250 AGTTGCTGTGTGAAGGCAATCATCTCTTCAATCCAGACATACGCGGCTCTGAAATGTC 1309
Qy 1647 GGGCGGAGATCGAGATGCGCGGAGAAAGGTGTACGCTTGTGCGAGGAGCATCTGCGGCC 1706
Db 1310 GAGCGGAGCTCGAGGTATGCTGGAATAATCTATGCTGTCTGGAAGACATCTGCCGCA 1369
Qy 1707 TGGAAATCCCGGCGAGCATGGAGCGCTTTGCGCAACTGCTGCTGCTGCGGCTTTCG 1766
Db 1370 CAGAACTCCAGGTGATGAGCGGCTTTGCTCAGCTACTACTAAAGTTGCGCGCATTCG 1429
Qy 1767 GATGATCAGGCTGAAAGTGGCAGGATCACTGTTCTCTTCCGATATTACGAGCCACCGGC 1826
Db 1430 GTTCCATCAGTCTCAAAATGCTCGATCATTTGTTTTCCTCCGTTTAAATAGCGCAAGAG 1489

QY 1827 CGCTGGAGGAGCTCTTTCTCGAGCAGCTGGAGGGCC 1863
Db 1490 CATTGGAGGAATTAAATTGCTGAGCAATTGGAGCTCC 1526

Search completed: May 22, 2006, 02:19:46
Job time : 1428 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 13:46:20 ; Search time 197 Seconds
(without alignments)
1179.015 Million cell updates/sec

Title: US-10-719-024-2

Perfect score: 2666
Sequence: 1 MNCQDASFRLSHIKEVK.....ELFLQLAPPPGLAMKLE 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2666	100.0	508	4	ABB60596
2	2666	100.0	508	9	ADY61075
3	2666	100.0	508	9	ABE53799
4	2661	99.8	508	9	ADY61100
5	2661	99.8	508	9	ADY61112
6	2661	99.8	508	9	ADY61098
7	2661	99.8	508	9	ADY61097
8	2660	99.8	508	9	ADY61111
9	2659	99.7	508	9	ADY61110
10	2658	99.7	508	9	ADY61101
11	2657	99.7	508	9	ADY61109
12	2656	99.6	508	9	ADY61099
13	2656	99.6	508	9	ADY61103
14	2656	99.6	508	9	ADY61102
15	2655	99.6	508	9	ADY61113
16	2646	99.2	508	9	ADY61108
17	2646	99.2	508	9	ADY61104
18	2634	98.8	508	9	ADY61106
19	2634	98.8	508	9	ADY61105
20	2624	98.4	508	9	ADY61107
21	2429	91.1	513	2	AAR14304
22	2429	91.1	513	2	AAR48065
23	2429	91.1	513	2	AAW18876

ALIGNMENTS

24	2429	91.1	513	2	AAW31320	AAW31320 D. melano
25	1728.5	64.8	467	4	AA67097	AA67097 L. cuprina
26	1728.5	64.8	467	4	AA67098	AA67098 L. cuprina
27	1728.5	64.8	467	4	AA67099	AA67099 L. cuprina
28	1609.5	60.4	458	2	AA28604	AA28604 L. cuprin
29	1309.5	49.1	448	6	ABU67310	ABU67310 Flea ultr
30	1309.5	49.1	448	6	ABU67309	ABU67309 Flea ultr
31	1309.5	49.1	448	6	ADU48276	ADU48276 Ctenoceph
32	1309.5	49.1	448	6	ADU48279	ADU48279 Ctenoceph
33	1309.5	49.1	474	6	ABU67311	ABU67311 Flea ultr
34	1309.5	49.1	474	6	ABU67312	ABU67312 Flea ultr
35	1309.5	49.1	474	8	ADU48285	ADU48285 Ctenoceph
36	1309.5	49.1	474	8	ADU48282	ADU48282 Ctenoceph
37	1097.5	41.2	460	3	AAV87471	AAV87471 European
38	1096.5	41.1	472	4	AAU10279	AAU10279 Spruce bu
39	1073.5	40.3	420	6	AAE30111	AAE30111 Heliothis
40	1071.5	40.2	466	5	ABB08661	ABB08661 Heliothis
41	1071.5	40.2	466	5	ABB08673	ABB08673 Heliothis
42	1058.5	39.7	467	8	ADR48590	ADR48590 Protein s
43	1058.5	39.7	490	8	ADR48552	ADR48552 Moltling h
44	1000	37.5	496	4	AA67107	AA67107 B tabaci
45	985	36.9	462	6	AAO30082	AAO30082 Human ret

RESULT 1
ID ABB60596
ABB60596 standard; protein; 508 AA.
XX
AC ABB60596;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 8580.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PERK) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR MPI: 2001-655660/75.
XX
DR N-PSDB; ABU04659.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
PS Disclosure; SEQ ID NO 8580; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signaling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
XX sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly

CC from wipo at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 508 AA;

Query Match 100.0%; Score 2666; DB 4; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.5e-201;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDNCDQDASFLSHIKKEVKPDIISQNDNNSSSPKAKESPVPFMQAMSMVHLPGNSA 60
DB 1 MDNCDQDASFLSHIKKEVKPDIISQNDNNSSSPKAKESPVPFMQAMSMVHLPGNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYOOQYPPNHPISGSKHLCSICGDRASGKHGYYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYOOQYPPNHPISGSKHLCSICGDRASGKHGYYS 120
QY 121 CEGCKGFPEKRTVRKDLTYACRENRCIIDKRQRNRCQYCRYOKCLTCGKREAVOEEROR 180
DB 121 CEGCKGFPEKRTVRKDLTYACRENRCIIDKRQRNRCQYCRYOKCLTCGKREAVOEEROR 180
QY 181 GARNNAAGRLSASGGSSGPGSVGSSSSQGGGGGGGSGVSGMGSGNGSDDPMTNVSRRPSI 240
DB 181 GARNNAAGRLSASGGSSGPGSVGSSSSQGGGGGGGSGVSGMGSGNGSDDPMTNVSRRPSI 240
QY 241 ERITAEQRAETOCGDRALTFRLVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 ERITAEQRAETOCGDRALTFRLVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 301 HPAQVPLDDQVILLKAAWIELLIANVAVCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360
DB 301 HPAQVPLDDQVILLKAAWIELLIANVAVCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360
QY 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLMDRRELSCLKAIIILYNPDI 420
DB 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLMDRRELSCLKAIIILYNPDI 420
QY 421 RGIKSRARIEEMCREKRYVACLDEHCRLHEPGDDGRFAOILLRLPALRSISLKCQDHLFLFR 480
DB 421 RGIKSRARIEEMCREKRYVACLDEHCRLHEPGDDGRFAOILLRLPALRSISLKCQDHLFLFR 480
QY 481 ITSDRPLELFLBQLEAPPPLGLAMKLE 508
DB 481 ITSDRPLELFLBQLEAPPPLGLAMKLE 508

RESULT 2
ADY61075
ID ADY61075 standard; protein; 508 AA.
XX
XX ADY61075;
XX
DB 19-MAY-2005 (first entry)
XX
XX D melanogaster ultraespirlacle (usp) wild-type protein SegID2.
XX
XX protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX
XX ultraespirlacle; USP.
XX
XX Drosophila melanogaster.
XX
XX US200504569-A1.
XX
XX PN 10-MAR-2005.
XX
XX PD 24-NOV-2003; 2003US-00719024.
XX
XX PF 22-NOV-2002; 2002US-0428282P.
XX
XX PR (JONE/) JONES G.
XX
XX PA (JONE/) JONES D.
XX
XX PI Jones G, Jones D;
XX
XX

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DR WPI; 2005-221953/23.
 DR N-PSDB; ADY61074.
 XX
 XX PT New mutant hormone receptor nucleic acids useful in the fields of drug
 PT discovery and pest control, in particular for identifying chemical
 PT compounds in activating or blocking particular hormone-dependent pathways
 PT in various organisms.
 XX
 XX PS Claim 1, SEQ ID NO 2; 35pp; English.

CC This invention relates to novel mutant nuclear hormone receptors and the
 CC DNA sequences which encode them. The invention may be useful for the
 CC development of compounds with a pesticide activity acting as hormone
 CC receptor agonists or antagonists. The methods and compositions of the
 CC present invention are useful in the fields of drug discovery and pest
 CC control, in particular for providing biochemical tools and assays to
 CC identify ligands of nuclear hormone receptors and identifying a pest
 CC control agent. The present sequence is that of the D melanogaster
 CC ultraespirlacle (usp) wild-type protein which was used during the
 CC development of the novel mutant nuclear hormone receptors of the
 CC invention.

Sequence 508 AA;

Query Match 100.0%; Score 2666; DB 9; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.5e-201;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDNCDQDASFLSHIKKEVKPDIISQNDNNSSSPKAKESPVPFMQAMSMVHLPGNSA 60
DB 1 MDNCDQDASFLSHIKKEVKPDIISQNDNNSSSPKAKESPVPFMQAMSMVHLPGNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYOOQYPPNHPISGSKHLCSICGDRASGKHGYYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYOOQYPPNHPISGSKHLCSICGDRASGKHGYYS 120
QY 121 CEGCKGFPEKRTVRKDLTYACRENRCIIDKRQRNRCQYCRYOKCLTCGKREAVOEEROR 180
DB 121 CEGCKGFPEKRTVRKDLTYACRENRCIIDKRQRNRCQYCRYOKCLTCGKREAVOEEROR 180
QY 181 GARNNAAGRLSASGGSSGPGSVGSSSSQGGGGGGGSGVSGMGSGNGSDDPMTNVSRRPSI 240
DB 181 GARNNAAGRLSASGGSSGPGSVGSSSSQGGGGGGGSGVSGMGSGNGSDDPMTNVSRRPSI 240
QY 241 ERITAEQRAETOCGDRALTFRLVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 ERITAEQRAETOCGDRALTFRLVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 301 HPAQVPLDDQVILLKAAWIELLIANVAVCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360
DB 301 HPAQVPLDDQVILLKAAWIELLIANVAVCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360
QY 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLMDRRELSCLKAIIILYNPDI 420
DB 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLMDRRELSCLKAIIILYNPDI 420
QY 421 RGIKSRARIEEMCREKRYVACLDEHCRLHEPGDDGRFAOILLRLPALRSISLKCQDHLFLFR 480
DB 421 RGIKSRARIEEMCREKRYVACLDEHCRLHEPGDDGRFAOILLRLPALRSISLKCQDHLFLFR 480
QY 481 ITSDRPLELFLBQLEAPPPLGLAMKLE 508
DB 481 ITSDRPLELFLBQLEAPPPLGLAMKLE 508

```

RESULT 3
 AEB53799
 ID AEB53799 standard; protein; 508 AA.
 XX
 XX AEB53799;
 XX
 XX 06-OCT-2005 (first entry)
 XX

DE Drosophila nuclear receptor #14.
 XX Insecticide; pesticide; toxin; nuclear receptor; receptor.
 XX Drosophila melanogaster.
 OS WO2005069859-A2.
 PN 04-AUG-2005.
 PD 13-JAN-2005; 2005WO-US001218.
 XX 13-JAN-2004; 2004US-0536337P.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Thummel CS, King-Jones K, Horner M, Lam G;
 PI WPI; 2005-555376/56.
 DR N-PSDB; AEB53800.
 XX Composition useful for increasing effect of existing toxins to control
 PT insect, and for inhibiting insect growth, comprises inhibitor of DHR96
 PT activity, and optionally pesticide.
 PS Disclosure; SEQ ID NO 27; 211pp; English.
 XX The invention relates to a composition comprising an inhibitor of DHR96
 CC activity and optionally a pesticide. The invention also relates to an
 CC insect comprising a gene, where the gene comprises a non-naturally
 CC occurring mutation in the DHR96 gene, a method of enhancing the effect a
 CC pesticide has on an insect involving administering to the insect an
 CC inhibitor of DHR96 activity, a method of identifying an inhibitor of
 CC DHR96 activity involving testing compounds for inhibiting activity of
 CC DHR96 and/or inhibition of xenobiotic activity and comparing the activity
 CC of these compounds to known inhibitors of DHR96, a method of producing a
 CC composition for inhibiting DHR96 activity involving admixing the
 CC inhibitor with a pesticide and a composition produced by the method. The
 CC composition and method are useful for enhancing the effect a pesticide
 CC has on an insect, for identifying an inhibitor of DHR96 activity, for
 CC identifying ligands for DHR96 and for producing a composition for
 CC inhibiting DHR96 activity. The composition is useful for regulating
 CC DHR96, preferably for inhibiting DHR96 gene expression or activity and
 CC for increasing the effect of existing toxins or pesticides e.g., DDT to
 CC control insects. The composition is useful for controlling insects e.g.,
 CC silverfish, dragonflies, stoneflies, beetles, fleas, ants, bees, wasps,
 CC termites etc. and decreases the resistance exhibited by the insects with
 CC respect to toxins or pesticides. This sequence represents a Drosophila
 CC nuclear receptor used in the scope of the invention.
 XX Sequence 508 AA;
 SQ
 Query Match 100.0%; Score 2666; DB 9; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.5e-201;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 ERIIEAEGRAETQCCDRALTFPLRVGPYSTVOPDYKGAVALCQVVKQLFQWVEYARBMMP 300
 QY 301 HFAQVPLDDQVILLAAWTELLIANVAMCSYSLDDGAGGGGGGLGHDGSTERPSPGIQ 360
 DB 301 HFAQVPLDDQVILLAAWTELLIANVAMCSYSLDDGAGGGGGGLGHDGSTERPSPGIQ 360
 QY 361 POOLFANOSFSYHRNSATKAGVSALFDRLTSELVYMKRLNDRBELSGLKATILYNPPI 420
 DB 361 POOLFANOSFSYHRNSATKAGVSALFDRLTSELVYMKRLNDRBELSGLKATILYNPPI 420
 QY 421 RGIKSRABIEMCREKYVACLDEHCRLEHPGDDGRRFAQLLRLPALRSISLKCQDHLFLRR 480
 DB 421 RGIKSRABIEMCREKYVACLDEHCRLEHPGDDGRRFAQLLRLPALRSISLKCQDHLFLRR 480
 QY 481 ITSDRPLEELFLEQLAAPPPLGAMKLR 508
 DB 481 ITSDRPLEELFLEQLAAPPPLGAMKLR 508
 RESULT 4
 ADY61100
 ID ADY61100 standard; protein; 508 AA.
 AC ADY61100;
 XX 19-MAY-2005 (first entry)
 DT D melanogaster ultraspiracle (USP) F302W mutant protein #4.
 XX protein engineering; hormone; pesticide; pharmaceutical; plant pest;
 KW ultraspiracle; USP; mutant; mutein.
 XX Drosophila melanogaster.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 302
 FT Misc-difference /note= "wild-type Phe replaced by Trp"
 PN US2005054569-A1.
 XX 10-MAR-2005.
 PD 24-NOV-2003; 2003US-00719024.
 XX 22-NOV-2002; 2002US-0428282P.
 PR (JONE/) JONES G.
 PA (JONE/) JONES D.
 PI Jones G, Jones D;
 DR WPI; 2005-221953/23.
 XX New mutant hormone receptor nucleic acids useful in the fields of drug
 PT discovery and pest control, in particular for identifying chemical
 PT compounds in activating or blocking particular hormone-dependent pathways
 PT in various organisms.
 XX Claim 4; Page; 35pp; English.
 PS This invention relates to novel mutant nuclear hormone receptors and the
 CC DNA sequences which encode them. The invention may be useful for the
 CC development of compounds with a pesticide activity acting as hormone
 CC receptor agonists or antagonists. The methods and compositions of the
 CC present invention are useful in the fields of drug discovery and pest
 CC control, in particular for providing biochemical tools and assays to
 CC identify ligands of nuclear hormone receptors and identifying a pest
 CC control agent. The present sequence is that of a mutant form of the D
 CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
 CC nuclear hormone receptors of the invention. Note: The present sequence
 CC was created by the indexer using information given in the claims of the

CC specification.

SQ Sequence 508 AA;

Query Match	99.8%;	Score 2661;	DB 9;	Length 508;
Best Local Similarity	99.8%;	Pred. No. 3.8e-201;		
Matches 507;	Conservative	1;	Mismatches 0;	Indels 0;
			Gaps	0

QY	1	MDNCODPASFRLSHIKEEYKPDISOLUNDBNNSSFSFKASAPVPMOMAMSVHYLPCSNNA	60
Db	1	MDNCODPASFRLSHIKEEYKPDISOLUNDBNNSSFSFKASAPVPMOMAMSVHYLPCSNNA	60
QY	61	SSNNNSAGDAQMAQAPNSAGSGSAAAAVQOQYPPNHPLSGSKHLCSI CGBRASGKHGYVYS	120
Db	61	SSNNNSAGDAQMAQAPNSAGSGSAAAAVQOQYPPNHPLSGSKHLCSI CGBRASGKHGYVYS	120
QY	121	CEGCKGFFPKRYTKULTYACRENRNCTIDKQGNRQYCRYOKCTLCQMKREAVQEROR	180
Db	121	CEGCKGFFPKRYTKULTYACRENRNCTIDKQGNRQYCRYOKCTLCQMKREAVQEROR	180
QY	181	GARNNAGRISASAGSGSGSGSVGSSQSGGSGGAGYSGGWSGNQSGDPEMTNSVSRDFSI	240
Db	181	GARNNAGRISASAGSGSGSGSGSVGSSQSGGSGGAGYSGGWSGNQSGDPEMTNSVSRDFSI	240
QY	241	ERIIEABQPAETOCGRALPTLRVGEYSTYQDPYKQAVSALCOVYNKOLFQMYETIARMP	300
Db	241	ERIIEABQPAETOCGRALPTLRVGEYSTYQDPYKQAVSALCOVYNKOLFQMYETIARMP	300
QY	301	HRQAVPLDDOVLILKKAAMELILANVAMCSIVSLDDGAGAGGGGGLGHDSFERRSPGLQ	360
Db	301	HRQAVPLDDOVLILKKAAMELILANVAMCSIVSLDDGAGAGGGGGLGHDSFERRSPGLQ	360
QY	361	POOLFNQSPSTHRNSAIRAQVSAITDRILISELSVMMKRLNDRBELSCLKAILLYNPD1	420
Db	361	POOLFNQSPSTHRNSAIRAQVSAITDRILISELSVMMKRLNDRBELSCLKAILLYNPD1	420
QY	421	RGIKSPASABIEMCBEKYYACIDECRIEHPDGDGRFQOILRLPALNSISLKCQDHLFLFR	480
Db	421	RGIKSPASABIEMCBEKYYACIDECRIEHPDGDGRFQOILRLPALNSISLKCQDHLFLFR	480
QY	481	ITSDRPLBELFLBQLEAPPPGLAMKLE	508
Db	481	ITSDRPLBELFLBQLEAPPPGLAMKLE	508

RESULT 5	
ADY61112	
ID	ADY61112 standard; protein; 508 AA.
XX	
XX	
AC	ADY61112;
XX	
DT	19-MAY-2005 (first entry)
XX	
XX	
DE	D melanogaster ultraaspiracle (USP) L366A mutant protein #16.
XX	
KW	protein engineering; hormone; pesticide; pharmaceutical; plant pest
KW	ultraaspiracle; USP; mutant; mutuin.
XX	
OS	Drosophila melanogaster.
OS	Synthetic.
XX	
XX	
Key	Location/Qualifiers
FT	Misc-difference 366
FT	/note= "Wild-type Leu replaced by Ala"
XX	
FN	US2005054569-A1.
XX	
PD	10-MAR-2005.
XX	
XX	
PF	24-NOV-2003; 2003US-00719024.
XX	
XX	
PR	22-NOV-2002; 2002US-0428282P.
XX	

PA (JONE/) JONES G.
PA (JONE/) JONES D.
XX
XX
PI Jones G, Jones D;
XX
XX
DR WPI, 2005-221953/23.
XX
XX
XX New mutant hormone receptor nucleic acids useful in the fields of drug
PT discovery and pest control, in particular for identifying chemical
PT compounds in activating or blocking particular hormone-dependent pathways
PT in various organisms.
XX
XX Claim 20; Page; 35pp; English.

Sequence 508 AA;

Query Match	99.8%	Score 2661	DB 9	Length 508
Best Local Similarity	99.8%	Pred. No. 3.8e-201		
Matches 507; Conservative	0	Mismatches 1	Indels 0	Gaps 0

[illegible]

RESULT 6
ADY61098
ID ADY61098 standard; protein; 508 AA

```
XX AC ADY61098;
XX DT 19-MAY-2005 (first entry)
XX DE D melanogaster ultraspiracle (USP) P479W mutant protein #2.
XX KM protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX KM ultraspiracle; USP; mutant; mutein.
XX OS Drosophila melanogaster.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 479
XX FT /note= "Wild-type Phe replaced by Trp"
XX PN US2005054569-A1.
XX PD 10-MAR-2005.
XX PF 24-NOV-2003; 2003US-00719024.
XX PR 22-NOV-2002; 2002US-0428282P.
XX PA (JONE/) JONES G.
XX PA (JONE/) JONES D.
XX PI Jones G, Jones D;
XX DR WPI; 2005-221953/23.
XX PT New mutant hormone receptor nucleic acids useful in the fields of drug
XX PT discovery and pest control, in particular for identifying chemical
XX PT compounds in activating or blocking particular hormone-dependent pathways
XX PT in various organisms.
XX PS Claim 3; Page; 35pp; English.
XX CC This invention relates to novel mutant nuclear hormone receptors and the
XX CC DNA sequences which encode them. The invention may be useful for the
XX CC development of compounds with a pesticide activity acting as hormone
XX CC receptor agonists or antagonists. The methods and compositions of the
XX CC present invention are useful in the fields of drug discovery and pest
XX CC control, in particular for providing biochemical tools and assays to
XX CC identify ligands of nuclear hormone receptors and identifying a pest
XX CC control agent. The present sequence is that of a mutant form of the D
XX CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
XX CC nuclear hormone receptors of the invention. Note: The present sequence
XX CC was created by the indexer using information given in the claims of the
XX CC specification.
SQ Sequence 508 AA;

Query Match          99.8%; Score 2661; DB 9; Length 508;
Best Local Similarity 99.8%; Pred. No. 3.8e-201;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 241 ERIIEAQRARETQCGDRALTPRVGPYSTVOPDYGAVALCOVYNKOLFQWEYARMP 300
DB 241 ERIIEAQRARETQCGDRALTPRVGPYSTVOPDYGAVALCOVYNKOLFQWEYARMP 300
QY 301 HFAQVPLDDQVILLKRAWIELLIANVAMCSIVSLDDGAGGGGGIGHDGSEFRSPGLQ 360
DB 301 HFAQVPLDDQVILLKRAWIELLIANVAMCSIVSLDDGAGGGGGIGHDGSEFRSPGLQ 360
QY 361 POOLFPLNGSPSYHRNSAIVAGVSAIFDRILSELVYMKRLNDRRELSTLKAIIIVNPD 420
DB 361 POOLFPLNGSPSYHRNSAIVAGVSAIFDRILSELVYMKRLNDRRELSTLKAIIIVNPD 420
QY 421 RGIKSRAREIEMCREKYVACTDEHCRLEHFGDDGFRFAOLLRLPALRSTLSLKCODHFLFR 480
DB 421 RGIKSRAREIEMCREKYVACTDEHCRLEHFGDDGFRFAOLLRLPALRSTLSLKCODHFLFR 480
QY 481 ITSDRPLBELFLEQLAAPPPLGAMKLE 508
DB 481 ITSDRPLBELFLEQLAAPPPLGAMKLE 508

RESULT 7
ID ADY61097 strand; protein; 508 AA.
XX AC ADY61097;
XX DT 19-MAY-2005 (first entry)
XX DE D melanogaster ultraspiracle (USP) P479W mutant protein #1.
XX KM protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX KM ultraspiracle; USP; mutant; mutein.
XX OS Drosophila melanogaster.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 477
XX FT /note= "Wild-type Phe replaced by Trp"
XX PN US2005054569-A1.
XX PD 10-MAR-2005.
XX PF 24-NOV-2003; 2003US-00719024.
XX PR 22-NOV-2002; 2002US-0428282P.
XX PA (JONE/) JONES G.
XX PA (JONE/) JONES D.
XX PI Jones G, Jones D;
XX DR WPI; 2005-221953/23.
XX PT New mutant hormone receptor nucleic acids useful in the fields of drug
XX PT discovery and pest control, in particular for identifying chemical
XX PT compounds in activating or blocking particular hormone-dependent pathways
XX PT in various organisms.
XX PS Claim 2; Page; 35pp; English.
XX CC This invention relates to novel mutant nuclear hormone receptors and the
XX CC DNA sequences which encode them. The invention may be useful for the
XX CC development of compounds with a pesticide activity acting as hormone
XX CC receptor agonists or antagonists. The methods and compositions of the
XX CC present invention are useful in the fields of drug discovery and pest
XX CC control, in particular for providing biochemical tools and assays to
XX CC identify ligands of nuclear hormone receptors and identifying a pest
XX CC control agent. The present sequence is that of a mutant form of the D
XX CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
```

CC nuclear hormone receptors of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.

XX Sequence 508 AA;

Query Match 99.8%; Score 2661; DB 9; Length 508;

Best Local Similarity 99.8%; Pred. No. 3.8e-201;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

DB 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

QY 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

DB 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

QY 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

DB 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

QY 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

DB 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

QY 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

DB 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

QY 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

DB 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

QY 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

DB 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

QY 421 RGIKRAEIMCREKRYVACLDEHCHLEHGGDGRFAOLLRLPALRSISLKCQDHLFLFR 480

DB 421 RGIKRAEIMCREKRYVACLDEHCHLEHGGDGRFAOLLRLPALRSISLKCQDHLFLFR 480

QY 481 ITSDRPLEBELFLEQLEAPPPLGIAWKLE 508

DB 481 ITSDRPLEBELFLEQLEAPPPLGIAWKLE 508

RESULT 8

ADY61111

ID ADY61111 standard; protein; 508 AA.

XX ADY61111;

XX 19-MAY-2005 (first entry)

XX D melanogaster ultraaspiracle (USP) Q288A mutant protein #15.

XX protein engineering; hormone; pesticide; pharmaceutical; plant pest;

XX ultraaspiracle; USP; mutant; mutein.

XX Drosophila melanogaster.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 288 /note="Wild-type Gln replaced by Ala"

XX US2005054569-A1.

XX 10-MAR-2005.

XX 24-NOV-2003; 2003US-00719024.

PR 22-NOV-2002; 2002US-0428282P.

XX (JONE/) JONES G.

XX (JONE/) JONES D.

XX Jones G, Jones D;

XX WPI, 2005-221953/23.

XX New mutant hormone receptor nucleic acids useful in the fields of drug

XX discovery and pest control, in particular for identifying chemical

XX compounds in activating or blocking particular hormone-dependent pathways

XX in various organisms.

XX Claim 19; Page; 35pp; English.

XX This invention relates to novel mutant nuclear hormone receptors and the

XX DNA sequences which encode them. The invention may be useful for the

XX development of compounds with a pesticide activity acting as hormone

XX receptor agonists or antagonists. The methods and compositions of the

XX present invention are useful in the fields of drug discovery and pest

XX control, in particular for providing biochemical tools and assays to

XX identify ligands of nuclear hormone receptors and identifying a pest

XX control agent. The present sequence is that of a mutant form of the D

XX melanogaster ultraaspiracle (USP) protein which represents a novel mutant

XX nuclear hormone receptors of the invention. Note: The present sequence

XX was created by the indexer using information given in the claims of the

XX specification.

XX Sequence 508 AA;

XX Query Match 99.8%; Score 2660; DB 9; Length 508;

XX Best Local Similarity 99.8%; Pred. No. 4.6e-201;

XX Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

DB 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

QY 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

DB 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

QY 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

DB 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

QY 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

DB 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

QY 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

DB 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

QY 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

DB 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

QY 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

DB 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

QY 421 RGIKRAEIMCREKRYVACLDEHCHLEHGGDGRFAOLLRLPALRSISLKCQDHLFLFR 480

CC nuclear hormone receptors of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.

XX Sequence 508 AA;

XX Query Match 99.8%; Score 2660; DB 9; Length 508;

XX Best Local Similarity 99.8%; Pred. No. 4.6e-201;

XX Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

DB 1 MDNCQDASFLRSHIKEEVKPDISQINDSNSSFPKAESEVPMQAMSMVHVLPGNSA 60

QY 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

DB 61 SSNNNSAGDAQMAOPNSAGSSAAAQVQOYPNNHPLSGSKLCSICGRASGKHGYYS 120

QY 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

DB 121 CEGCKGFPRKTVRKDLYACRENRCIIDKQRNRCQYCRYOKCLTCGKREAVOEERQ 180

QY 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

DB 181 GARNAAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSNGSDDFMTNSVRDPSI 240

QY 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

DB 241 BRITAEORAEETQCGDRALTLFRVGPYSTVOPDYKGAVALCOVNNKOLFQWVEYARAMP 300

QY 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

DB 301 HPAQVPLDDOYITLKAAMIELLIANVAMCSIVSLDDGAGGGGGGLGHDGSPERRSPGLQ 360

QY 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

DB 361 POOLFNGSFYHRNSAIKAGVSAIFDRITLSELVYMKRLNDRRELCLKAIILYNPDI 420

QY 421 RGIKRAEIMCREKRYVACLDEHCHLEHGGDGRFAOLLRLPALRSISLKCQDHLFLFR 480

DB 421 RGIKRAEIMCREKRYVACLDEHCHLEHGGDGRFAOLLRLPALRSISLKCQDHLFLFR 480

QY 481 ITSDRPLEBELFLEQLEAPPPLGIAWKLE 508

DB 481 ITSDRPLEBELFLEQLEAPPPLGIAWKLE 508

RESULT 9

ADY61110
 ID ADY61110 standard; protein; 508 AA.
 AC ADY61110;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE D melanogaster ultraaspiracle (USP) V293R mutant protein #14.
 XX
 KW protein engineering; hormone; pesticide; pharmaceutical; plant pest;
 KM ultraaspiracle; USP; mutant; mutein.
 XX
 OS Drosophila melanogaster.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 293 /note="Wild-type Val replaced by Arg"
 FT
 XX
 PN US2005054569-A1.
 XX
 PD 10-MAR-2005.
 XX
 XX 24-NOV-2003; 2003US-00719024.
 PF
 XX
 PR 22-NOV-2002; 2002US-0428282P.
 XX
 PA (JONE/) JONES G.
 PA (JONE/) JONES D.
 XX
 PI Jones G, Jones D;
 XX
 DR WPI: 2005-221953/23.
 XX
 PT New mutant hormone receptor nucleic acids useful in the fields of drug
 PT discovery and pest control, in particular for identifying chemical
 PT compounds in activating or blocking particular hormone-dependent pathways
 PT in various organisms.
 XX
 PS Claim 18; Page; 35pp; English.
 XX
 CC This invention relates to novel mutant nuclear hormone receptors and the
 CC DNA sequences which encode them. The invention may be useful for the
 CC development of compounds with a pesticide activity acting as hormone
 CC receptor agonists or antagonists. The methods and compositions of the
 CC present invention are useful in the fields of drug discovery and pest
 CC control, in particular for providing biochemical tools and assays to
 CC identify ligands of nuclear hormone receptors and identifying a pest
 CC control agent. The present sequence is that of a mutant form of the D
 CC melanogaster ultraaspiracle (USP) protein which represents a novel mutant
 CC nuclear hormone receptors of the invention. Note: The present sequence
 CC was created by the indexer using information given in the claims of the
 CC specification.
 CC
 XX
 SQ Sequence 508 AA;
 XX
 XX
 Query Match 99.7%; Score 2659; DB 9; Length 508;
 Best Local Similarity 99.8%; Pred. No. 5.5e-201;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDNCQDASFLSHKEVKPDISQJLNDSSNNSFPSPKASPPVFMQAMSMVTLPGNSNA 60
 DB 1 MDNCQDASFLSHKEVKPDISQJLNDSSNNSFPSPKASPPVFMQAMSMVTLPGNSNA 60
 QY 61 SSNNNSAGDQMAQPNASGSAALAAVQOQPPNHPHLSGSKHLGICDPRASGKHGYYS 120
 DB 61 SSNNNSAGDQMAQPNASGSAALAAVQOQPPNHPHLSGSKHLGICDPRASGKHGYYS 120
 QY 121 CEGCGFPRKRTYRKULTYACRENRCIIDKROBNRCYCRVOKCLTCGMKEAAVGEEROR 180
 DB 121 CEGCGFPRKRTYRKULTYACRENRCIIDKROBNRCYCRVOKCLTCGMKEAAVGEEROR 180
 QY 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDDPMTNSVSRDPSI 240

DB 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDDPMTNSVSRDPSI 240
 QY 241 ERIIEAEOQAEFOCCDRALTFLRVGPYSTVQPDYGAVALCOVYNKOLFQWETARMP 300
 DB 241 ERIIEAEOQAEFOCCDRALTFLRVGPYSTVQPDYGAVALCOVYNKOLFQWETARMP 300
 QY 301 HPAQVPLDDQVILLKAAWIELLIANVAMCSIVSLDDGGAGGGGGGLGHDSFERRSPGIQ 360
 DB 301 HPAQVPLDDQVILLKAAWIELLIANVAMCSIVSLDDGGAGGGGGGLGHDSFERRSPGIQ 360
 QY 361 POOLFANOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLNDRRELSCAKAIIILYNPDI 420
 DB 361 POOLFANOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLNDRRELSCAKAIIILYNPDI 420
 QY 421 RKIKRAEIEMCREYVACLDHCKLHPGDDGRFAQLILRLPALRSISLCKODHLFLRR 480
 DB 421 RKIKRAEIEMCREYVACLDHCKLHPGDDGRFAQLILRLPALRSISLCKODHLFLRR 480
 QY 481 ITSDRPLEELFLEQLAAPPPLAMKLE 508
 DB 481 ITSDRPLEELFLEQLAAPPPLAMKLE 508
 RESULT 10
 ADY61101
 ID ADY61101 standard; protein; 508 AA.
 AC ADY61101;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE D melanogaster ultraaspiracle (USP) K315W mutant protein #5.
 XX
 KW protein engineering; hormone; pesticide; pharmaceutical; plant pest;
 KW ultraaspiracle; USP; mutant; mutein.
 XX
 OS Drosophila melanogaster.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 315 /note="Wild-type Lys replaced by Trp"
 FT
 XX
 PN US2005054569-A1.
 XX
 PD 10-MAR-2005.
 XX
 PF 24-NOV-2003; 2003US-00719024.
 XX
 PR 22-NOV-2002; 2002US-0428282P.
 XX
 PA (JONE/) JONES G.
 PA (JONE/) JONES D.
 XX
 PI Jones G, Jones D;
 XX
 DR WPI: 2005-221953/23.
 XX
 PT New mutant hormone receptor nucleic acids useful in the fields of drug
 PT discovery and pest control, in particular for identifying chemical
 PT compounds in activating or blocking particular hormone-dependent pathways
 PT in various organisms.
 XX
 PS Claim 5; Page; 35pp; English.
 XX
 CC This invention relates to novel mutant nuclear hormone receptors and the
 CC DNA sequences which encode them. The invention may be useful for the
 CC development of compounds with a pesticide activity acting as hormone
 CC receptor agonists or antagonists. The methods and compositions of the
 CC present invention are useful in the fields of drug discovery and pest
 CC control, in particular for providing biochemical tools and assays to
 CC identify ligands of nuclear hormone receptors and identifying a pest

CC control agent. The present sequence is that of a mutant form of the D
CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
CC nuclear hormone receptors of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.

XX
XX
SQ Sequence 508 AA;

Query Match 99.7%; Score 2658; DB 9; Length 508;

Best Local Similarity 99.8%; Pred. No. 6.6e-201; Indels 0; Gaps 0;

Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDNCQDASFLRSHIKKEVKPDISQNDNSNNSFSPKASVPPFMQAMSMVHLPGNSA 60
DB 1 MDNCQDASFLRSHIKKEVKPDISQNDNSNNSFSPKASVPPFMQAMSMVHLPGNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSAAAQVQYPPNHPPLSGSKLCSICGDRASGKHYGYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSAAAQVQYPPNHPPLSGSKLCSICGDRASGKHYGYS 120
QY 121 CEGCKGFFKRTVTKDLYACRENRCIIDKQRNRCQYCRQYKCLTCGKREAVQEEQR 180
DB 121 CEGCKGFFKRTVTKDLYACRENRCIIDKQRNRCQYCRQYKCLTCGKREAVQEEQR 180
QY 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDPFMTNSVRDSI 240
DB 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDPFMTNSVRDSI 240
QY 241 BRITAEQRAETQCGDRALTLRVGPYSTVQPDYKAVSALCOVYNNKOLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTLRVGPYSTVQPDYKAVSALCOVYNNKOLFQWVEYARAMP 300
QY 301 HPAQVPLDDQVTLTKAAMTELLIANVAMCSIVSLDDGAGGGGGGIGHGSPERRSPGLQ 360
DB 301 HPAQVPLDDQVTLTKAAMTELLIANVAMCSIVSLDDGAGGGGGGIGHGSPERRSPGLQ 360
QY 361 POOLFINSFSYHNSAIKAGVSAIFDRITSELVYMKRLNDRRELSCLAIIILYNPDI 420
DB 361 POOLFINSFSYHNSAIKAGVSAIFDRITSELVYMKRLNDRRELSCLAIIILYNPDI 420
QY 421 RGKISRABIEKREKRYVACLDHCRLEHPGDDGRFAQLLRPLALRSISLKCQDHLFLR 480
DB 421 RGKISRABIEKREKRYVACLDHCRLEHPGDDGRFAQLLRPLALRSISLKCQDHLFLR 480
QY 481 ITSDRPLEELFLEOLEAPPPGLAMKLE 508
DB 481 ITSDRPLEELFLEOLEAPPPGLAMKLE 508

RESULT 11

ADY61109
ID ADY61109 standard; protein; 508 AA.

XX
XX
AC ADY61109;

XX
XX
DT 19-MAY-2005 (first entry)

XX
XX
DE D melanogaster ultraspiracle (USP) F302R mutant protein #13.

XX
XX
KW protein engineering; hormone; pesticide; pharmaceutical; plant pest;

XX
XX
KM ultraspiracle; USP; mutant; mutein.

OS
OS
OS Drosophila melanogaster.

OS
OS
OS Synthetic.

XX
XX
FH Key Location/Qualifiers

FT Misc-difference 302

FT /note= "Wild-type Phe replaced by Arg"

XX
XX
PM US2005054569-A1.

XX
XX
PD 10-MAR-2005.

PF 24-NOV-2003; 2003US-00719024.

XX
XX
PR 22-NOV-2002; 2002US-0428282P.

XX
XX
PA (JONES/) JONES G.

PA (JONES/) JONES D.

XX
XX
PI Jones G, Jones D;

XX
XX
DR WPI, 2005-221953/23.

XX
XX
PT New mutant hormone receptor nucleic acids useful in the fields of drug

PT discovery and pest control, in particular for identifying chemical

PT compounds in activating or blocking particular hormone-dependent pathways

PT in various organisms.

PS Claim 17; Page; 35pp; English.

CC This invention relates to novel mutant nuclear hormone receptors and the
CC DNA sequences which encode them. The invention may be useful for the
CC development of compounds with a pesticide activity acting as hormone
CC receptor agonists or antagonists. The methods and compositions of the
CC present invention are useful in the fields of drug discovery and pest
CC control, in particular for providing biochemical tools and assays to
CC identify ligands of nuclear hormone receptors and identifying a pest
CC control agent. The present sequence is that of a mutant form of the D
CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
CC nuclear hormone receptors of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.

SQ Sequence 508 AA;

Query Match 99.7%; Score 2657; DB 9; Length 508;

Best Local Similarity 99.8%; Pred. No. 7.9e-201; Indels 0; Gaps 0;

Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDNCQDASFLRSHIKKEVKPDISQNDNSNNSFSPKASVPPFMQAMSMVHLPGNSA 60
DB 1 MDNCQDASFLRSHIKKEVKPDISQNDNSNNSFSPKASVPPFMQAMSMVHLPGNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSAAAQVQYPPNHPPLSGSKLCSICGDRASGKHYGYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSAAAQVQYPPNHPPLSGSKLCSICGDRASGKHYGYS 120
QY 121 CEGCKGFFKRTVTKDLYACRENRCIIDKQRNRCQYCRQYKCLTCGKREAVQEEQR 180
DB 121 CEGCKGFFKRTVTKDLYACRENRCIIDKQRNRCQYCRQYKCLTCGKREAVQEEQR 180
QY 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDPFMTNSVRDSI 240
DB 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGSGVSGMGSGNGSDPFMTNSVRDSI 240
QY 241 BRITAEQRAETQCGDRALTLRVGPYSTVQPDYKAVSALCOVYNNKOLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTLRVGPYSTVQPDYKAVSALCOVYNNKOLFQWVEYARAMP 300
QY 301 HPAQVPLDDQVTLTKAAMTELLIANVAMCSIVSLDDGAGGGGGGIGHGSPERRSPGLQ 360
DB 301 HPAQVPLDDQVTLTKAAMTELLIANVAMCSIVSLDDGAGGGGGGIGHGSPERRSPGLQ 360
QY 361 POOLFINSFSYHNSAIKAGVSAIFDRITSELVYMKRLNDRRELSCLAIIILYNPDI 420
DB 361 POOLFINSFSYHNSAIKAGVSAIFDRITSELVYMKRLNDRRELSCLAIIILYNPDI 420
QY 421 RGKISRABIEKREKRYVACLDHCRLEHPGDDGRFAQLLRPLALRSISLKCQDHLFLR 480
DB 421 RGKISRABIEKREKRYVACLDHCRLEHPGDDGRFAQLLRPLALRSISLKCQDHLFLR 480
QY 481 ITSDRPLEELFLEOLEAPPPGLAMKLE 508
DB 481 ITSDRPLEELFLEOLEAPPPGLAMKLE 508

RESULT 12

ADY61099

ID ADY61099 standard; protein; 508 AA.

XX AC ADY61099;

DT 19-MAY-2005 (first entry)

DE D melanogaster ultraspiracle (USP) F477W/F479W mutant protein #3.

XX protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX ultraspiracle; USP; mutant; mutein.XX Drosophila melanogaster.
XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 477

FT /note= "Wild-type Phe replaced by Trp"

FT Misc-difference 479

FT /note= "Wild-type Phe replaced by Trp"

XX US2005054569-A1.

XX 10-MAR-2005.

XX 24-NOV-2003; 2003US-00719024.

XX 22-NOV-2002; 2002US-0428282P.

XX (JONE/) JONES G.

XX (JONE/) JONES D.

XX Jones G, Jones D;

XX WPI; 2005-221953/23.

XX New mutant hormone receptor nucleic acids useful in the fields of drug
XX discovery and pest control, in particular for identifying chemical
XX compounds in activating or blocking particular hormone-dependent pathways
XX in various organisms.

XX Claim 1; Page; 35pp; English.

XX This invention relates to novel mutant nuclear hormone receptors and the
XX DNA sequences which encode them. The invention may be useful for the
XX development of compounds with a pesticide activity acting as hormone
XX receptor agonists or antagonists. The methods and compositions of the
XX present invention are useful in the fields of drug discovery and pest
XX control, in particular for providing biochemical tools and assays to
XX identify ligands of nuclear hormone receptors and identifying a pest
XX control agent. The present sequence is that of a mutant form of the D
XX melanogaster ultraspiracle (USP) protein which represents a novel mutant
XX nuclear hormone receptors of the invention. Note: The present sequence
XX was created by the indexer using information given in the claims of the
XX specification.

XX Sequence 508 AA;

Query Match 99.6%; Score 2656; DB 9; Length 508;

Best Local Similarity 99.6%; Pred. No. 9.5e-201;

Matches 506; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDNCQDASFRLSHKEVKPDISQNDNSNSFSPKASPPVFNQAMSMVHLPFGSSNA 60

DB 1 MDNCQDASFRLSHKEVKPDISQNDNSNSFSPKASPPVFNQAMSMVHLPFGSSNA 60

QY 61 SSNNNSAGDQAOAPNSAGSAAAAYOOQVPPNPLSGSKHLCICGDRASGKRYGYS 120

DB 61 SSNNNSAGDQAOAPNSAGSAAAAYOOQVPPNPLSGSKHLCICGDRASGKRYGYS 120

QY 121 CEGCKGFFKRTVRKDLTYACRENRCIIDKQRNRCQYCRYOXKCLTCGKREAVQEROR 180

DB 121 CEGCKGFFKRTVRKDLTYACRENRCIIDKQRNRCQYCRYOXKCLTCGKREAVQEROR 180

QY 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGGGVSAGMGSGNSDDPMTNSVSRDPSI 240

DB 181 GARNAGRLSASGGSSGPGSVGSSSQGGGGGGGVSAGMGSGNSDDPMTNSVSRDPSI 240

QY 241 ERIIEAQRATFQCDBALTFPLRGVPSTVQPDYGAVALCQVYNNKOLFQVETARAMP 300

DB 241 ERIIEAQRATFQCDBALTFPLRGVPSTVQPDYGAVALCQVYNNKOLFQVETARAMP 300

QY 301 HFAQVPLDDQVILLKAAWTELLIANVAVCSIVSLDDGAGGGGGGIGHDGFERRSPGLQ 360

DB 301 HFAQVPLDDQVILLKAAWTELLIANVAVCSIVSLDDGAGGGGGGIGHDGFERRSPGLQ 360

QY 361 POQLFLOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLNDRRELSCAKIILYNPDI 420

DB 361 POQLFLOSFSYHRNSAIKAGVSAIFDRILSELVYMKRLNDRRELSCAKIILYNPDI 420

QY 421 RGIKSRATIEMCREKRYACLDHCRLEHPGDDGFAQLLRPALRSISLKCQDHLFLRR 480

DB 421 RGIKSRATIEMCREKRYACLDHCRLEHPGDDGFAQLLRPALRSISLKCQDHLFLRR 480

QY 481 ITSDBRPLEELFLEQLAAPPPLGLANKLR 508

DB 481 ITSDBRPLEELFLEQLAAPPPLGLANKLR 508

RESULT 13

ADY61103

ID ADY61103 standard; protein; 508 AA.

XX AC ADY61103;

DT 19-MAY-2005 (first entry)

DE D melanogaster ultraspiracle (USP) W328F mutant protein #7.

XX protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX ultraspiracle; USP; mutant; mutein.XX Drosophila melanogaster.
XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 328

FT /note= "Wild-type Trp replaced by Phe"

XX US2005054569-A1.

XX 10-MAR-2005.

XX 24-NOV-2003; 2003US-00719024.

XX 22-NOV-2002; 2002US-0428282P.

XX (JONE/) JONES G.

XX (JONE/) JONES D.

XX Jones G, Jones D;

XX WPI; 2005-221953/23.

XX New mutant hormone receptor nucleic acids useful in the fields of drug
XX discovery and pest control, in particular for identifying chemical
XX compounds in activating or blocking particular hormone-dependent pathways
XX in various organisms.

XX Claim 7; Page; 35pp; English.

XX This invention relates to novel mutant nuclear hormone receptors and the
XX DNA sequences which encode them. The invention may be useful for the
XX development of compounds with a pesticide activity acting as hormone

receptor agonists or antagonists. The methods and compositions of the present invention are useful in the fields of drug discovery and pest control, in particular for providing biochemical tools and assays to identify ligands of nuclear hormone receptors and identifying a pest control agent. The present sequence is that of a mutant form of the D melanogaster ultraspiracle (USP) protein which represents a novel mutant nuclear hormone receptor of the invention. Note: The present sequence was created by the indexer using information given in the claims of the specification.

Sequence 508 AA;

Query Match 99.6%; Score 2656; DB 9; Length 508;
Best Local Similarity 99.8%; Pred. No. 9.5e-201;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MDNCQDASFRLSHIKEVKRPDISQLDNNSSSPKAESEPPFMQMSMHWVLPGSNSA 60
DB 1 MDNCQDASFRLSHIKEVKRPDISQLDNNSSSPKAESEPPFMQMSMHWVLPGSNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYQOQYPPNHPLSGSKHLCSICGDRASGKHGYYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYQOQYPPNHPLSGSKHLCSICGDRASGKHGYYS 120
QY 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
DB 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
QY 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
DB 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
QY 161 GARNNAGRLSASGGSSGPGSVGGSSSQGGGGGSGVSGMGSGNSDDPMNTSVSRDPSI 240
DB 161 GARNNAGRLSASGGSSGPGSVGGSSSQGGGGGSGVSGMGSGNSDDPMNTSVSRDPSI 240
QY 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 301 HFAQVPLDDQVITLKAAMIETLLIANVAMCSIVSLDDGAGGGGGGLGHDGSEFERRSPGLQ 360
DB 301 HFAQVPLDDQVITLKAAMIETLLIANVAMCSIVSLDDGAGGGGGGLGHDGSEFERRSPGLQ 360
QY 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELSTYMKRLINDRRELSTCLAKIILYNDI 420
DB 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELSTYMKRLINDRRELSTCLAKIILYNDI 420
QY 421 RGIKSRRAETEMCREKVVYACLDHCRLEHGGDGRPAQLLRLPALRSISLKCQDHLFLFR 480
DB 421 RGIKSRRAETEMCREKVVYACLDHCRLEHGGDGRPAQLLRLPALRSISLKCQDHLFLFR 480
QY 481 ITSDBRPLEBELFLEOLEAPPPPGIANKLE 508
DB 481 ITSDBRPLEBELFLEOLEAPPPPGIANKLE 508
```

RESULT 14
ADY61102
ID ADY61102 standard; protein; 508 AA.

AC ADY61102;
DT 19-MAY-2005 (first entry)
DE D melanogaster ultraspiracle (USP) W318F mutant protein #6.

KM protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX ultraspiracle; USP; mutant; mutlein.

OS Drosophila melanogaster.
OS Synthetic.

XX Key location/Qualifiers
PH Misc-difference 318 /note= "Wild-type Trp replaced by Phe"
FT
XX

PN US2005054569-A1.

XX 10-MAR-2005.

XX 24-NOV-2003; 2003US-00719024.

PR 22-NOV-2002; 2002US-0428282P.

PA (JONE/) JONES G.

PA (JONE/) JONES D.

PI Jones G, Jones D;

DR WPI; 2005-221953/23.

PT New mutant hormone receptor nucleic acids useful in the fields of drug
PT discovery and pest control, in particular for identifying chemical
PT compounds in activating or blocking particular hormone-dependent pathways
PT in various organisms.

PS Claim 6; Page; 35pp; English.

CC This invention relates to novel mutant nuclear hormone receptors and the
CC DNA sequences which encode them. The invention may be useful for the
CC development of compounds with a pesticide activity acting as hormone
CC receptor agonists or antagonists. The methods and compositions of the
CC present invention are useful in the fields of drug discovery and pest
CC control, in particular for providing biochemical tools and assays to
CC identify ligands of nuclear hormone receptors and identifying a pest
CC control agent. The present sequence is that of a mutant form of the D
CC melanogaster ultraspiracle (USP) protein which represents a novel mutant
CC nuclear hormone receptor of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.

Sequence 508 AA;

Query Match 99.6%; Score 2656; DB 9; Length 508;
Best Local Similarity 99.8%; Pred. No. 9.5e-201;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MDNCQDASFRLSHIKEVKRPDISQLDNNSSSPKAESEPPFMQMSMHWVLPGSNSA 60
DB 1 MDNCQDASFRLSHIKEVKRPDISQLDNNSSSPKAESEPPFMQMSMHWVLPGSNSA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYQOQYPPNHPLSGSKHLCSICGDRASGKHGYYS 120
DB 61 SSNNNSAGDAQMAQAPNSAGSSAAAAYQOQYPPNHPLSGSKHLCSICGDRASGKHGYYS 120
QY 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
DB 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
QY 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
DB 121 CEGCKGFFKRTVTRKDLTYACRENRCIIDKQRNRCQYCRYOXCLTCGKREAVQEBQR 180
QY 161 GARNNAGRLSASGGSSGPGSVGGSSSQGGGGGSGVSGMGSGNSDDPMNTSVSRDPSI 240
DB 161 GARNNAGRLSASGGSSGPGSVGGSSSQGGGGGSGVSGMGSGNSDDPMNTSVSRDPSI 240
QY 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
DB 241 BRITAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVALCOVYNKQLFQWVEYARAMP 300
QY 301 HFAQVPLDDQVITLKAAMIETLLIANVAMCSIVSLDDGAGGGGGGLGHDGSEFERRSPGLQ 360
DB 301 HFAQVPLDDQVITLKAAMIETLLIANVAMCSIVSLDDGAGGGGGGLGHDGSEFERRSPGLQ 360
QY 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELSTYMKRLINDRRELSTCLAKIILYNDI 420
DB 361 POOLFNLNOSFSYHRNSAIKAGVSAIFDRILSELSTYMKRLINDRRELSTCLAKIILYNDI 420
QY 421 RGIKSRRAETEMCREKVVYACLDHCRLEHGGDGRPAQLLRLPALRSISLKCQDHLFLFR 480
DB 421 RGIKSRRAETEMCREKVVYACLDHCRLEHGGDGRPAQLLRLPALRSISLKCQDHLFLFR 480
```

QY 481 ITSDRPLEBFLFLEQLBAPPPGLAMKLE 508
DB 481 ITSDRPLEBFLFLEQLBAPPPGLAMKLE 508
RESULT 15
ID ADY61113 standard; protein; 508 AA.
XX
AC ADY61113;
XX
DT 19-MAY-2005 (first entry)
XX
DE D melanogaster ultrarespiracle (USP) Q288A/L366A mutant protein #17.
XX
KM protein engineering; hormone; pesticide; pharmaceutical; plant pest;
XX ultrarespiracle; USP; mutant; mutain.
OS Drosophila melanogaster.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 288 /note= "Wild-type Gln replaced by Ala"
FT Misc-difference 366 /note= "Wild-type Leu replaced by Ala"
XX
PN US2005054569-A1.
XX
PD 10-MAR-2005.
XX
PF 24-NOV-2003; 2003US-00719024.
XX
PR 22-NOV-2002; 2002US-0428282P.
XX
PA (JONE/) JONES G.
XX (JONE/) JONES D.
PI Jones G, Jones D;
XX
DR WPI; 2005-221953/23.
XX
PT New mutant hormone receptor nucleic acids useful in the fields of drug
PT discovery and pest control, in particular for identifying chemical
PT compounds in activating or blocking particular hormone-dependent pathways
PT in various organisms.
XX
PS Claim 21; Page; 35pp; English.
XX
CC This invention relates to novel mutant nuclear hormone receptors and the
CC DNA sequences which encode them. The invention may be useful for the
CC development of compounds with a pesticide activity acting as hormone
CC receptor agonists or antagonists. The methods and compositions of the
CC present invention are useful in the fields of drug discovery and pest
CC control, in particular for providing biochemical tools and assays to
CC identify ligands of nuclear hormone receptors and identifying a pest
CC control agent. The present sequence is that of a mutant form of the D
CC melanogaster ultrarespiracle (USP) protein which represents a novel mutant
CC nuclear hormone receptors of the invention. Note: The present sequence
CC was created by the indexer using information given in the claims of the
CC specification.
XX
SQ Sequence 508 AA;

Query Match 99.6%; Score 2655; DB 9; Length 508;
Best Local Similarity 99.6%; Pred. No. 1.1e-200;
Matches 506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNQCDDASFRLSHKEVYKPDISQNDSSSFPKASPPVFMQAMGMVHVLPGNSNA 60
DB 1 MNQCDDASFRLSHKEVYKPDISQNDSSSFPKASPPVFMQAMGMVHVLPGNSNA 60
QY 61 SSNNNSAGDAQMAQAPNSAGSAAAAVQOYPPNHPLSGSKHLCSICGDRASGKHVGYVS 120

DB 61 SSNNNSAGDAQMAQAPNSAGSAAAAVQOYPPNHPLSGSKHLCSICGDRASGKHVGYVS 120
QY 121 CEGCKGFFRRTYRKDLYACRENRNCITDKQRNRCQYCRYOXCLTCMKREAVQEBROR 180
DB 121 CEGCKGFFRRTYRKDLYACRENRNCITDKQRNRCQYCRYOXCLTCMKREAVQEBROR 180
QY 181 GARNAGRLSASGSGSGPGSVGSSQGGGGGGGVSGMGSGNGSDDPFMTNSVSRDFSI 240
DB 181 GARNAGRLSASGSGSGPGSVGSSQGGGGGGGVSGMGSGNGSDDPFMTNSVSRDFSI 240
QY 241 ERIIEAORAEITQCGDRALTLRVGPYSTVOPDYKAVSALCQVVKQLFQWVEYARMP 300
DB 241 ERIIEAORAEITQCGDRALTLRVGPYSTVOPDYKAVSALCQVVKQLFQWVEYARMP 300
QY 301 HFAQVPLDQVILLKAMTELLIANVAMCSIVSLDDGAGGGGGGIGHDGSFERRSPGLQ 360
DB 301 HFAQVPLDQVILLKAMTELLIANVAMCSIVSLDDGAGGGGGGIGHDGSFERRSPGLQ 360
QY 361 POOLFANOSFYHRNSAIKAGVSAIPDRILSLSVKMKRLNIDRRELSCIKATILYNPDI 420
DB 361 POOLFANOSFYHRNSAIKAGVSAIPDRILSLSVKMKRLNIDRRELSCIKATILYNPDI 420
QY 421 RGIKSRABIEIMCREKRYACLDEHCRLEHFGDDGRFAQLILRLPALRSISLKCQDHLFLFR 480
DB 421 RGIKSRABIEIMCREKRYACLDEHCRLEHFGDDGRFAQLILRLPALRSISLKCQDHLFLFR 480
QY 481 ITSDRPLEBFLFLEQLBAPPPGLAMKLE 508
DB 481 ITSDRPLEBFLFLEQLBAPPPGLAMKLE 508

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